A METHOD BASED ON CONSERVED MULTIPLE AMINO ACID PROPERTIES TO PREDICT AMINO ACID SUBSTITUTIONS WHICH MAINTAIN THE PROTEIN STRUCTURE

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A METHOD BASED ON CONSERVED MULTIPLE AMINO ACID PROPERTIES TO PREDICT AMINO ACID SUBSTITUTIONS WHICH MAINTAIN THE PROTEIN STRUCTURE

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Proteins often contain several domains, each with a distinct structure. Such domains have evolved as units that, when combined in various arrangements, produce proteins of unique structure. This study was conducted to identify amino acid substitutions that don't change structure. Amino acid properties which were conserved in proteins with identical structures were used to predict a set of amino acids profiles at each sequence position that can serve as viable substitutions. To test this analysis ten different protein sets were taken from the Conserved Domain Database of National Center for Biotechnology Information (NCBI). An amino acid index database of numerical indices representing various physicochemical and biochemical properties of amino acids were mapped onto the amino acid sequences in each dataset and these were used to select properties common to the proteins with the same structure. Based on these conserved properties, a substitution index percentage (SI%) was calculated to represent the relative ability of an amino acid to substitute at a given position and still maintain a protein structure. Amino acid profiles from different SI% ranges were used to create a set of substitutions into the consensus sequence of each dataset (AASCS). The AASCS from each SI% range were submitted to two validation programs, RPS-BLAST and PSI-PRED. The number of matches between

the AASCS and the primary data set sequences for each SI% range was used to select the substitution profile ranges that best maintained the structure. It was concluded that amino acid, substitutions with SI% greater than 90% consistently conserved the structure of the protein. This method may prove useful in predicting the structure of proteins with induced mutations (site-directed mutagenesis), and in studies pertaining to protein engineering.

Introduction

The tremendous explosion in the amount of genome sequences during the past few years has made available an overwhelming amount of functional and structural data for proteins. With this explosion has come the need to make functional and structural assignments to new sequences. The most common way of inferring the function of a protein is based on the sequence similarity with proteins of known function (Cuff *et al.,* 1999). Classic sequence comparison algorithms like BLAST (Altschul *et al*., 1990) were designed to assess the degree of sequence similarities between compared sequences (Dominique and Gilles, 2001; Rychlewski and Godzik, 1997). However an increasing number of proteins with weak sequence similarity have been found to assume similar three-dimensional (3D) folds, often with similar biochemical or biophysical functions (Igore and Sung, 1999). Therefore, these alignment methods are valuable tools for identifying sequences similar in function, but they are not as accurate in predicting the structure of a protein (Garnier. 1990; Frishman and Argos, 1997; Lin and Pan, 2001; Petersen *et al.,* 2000). The search for new and better methods for predicting the structure of proteins is currently the most researched area in the field of proteomics and bioinformatics.

Some proteins can be very tolerant to amino acid substitution, even within their core (Patrice and Michael, 1999). Understanding the factors responsible for this behavior is of critical importance for developing an understanding of protein structure conformation. Mutations in proteins have been quantified in terms of the changes in structural stability that they induce (Saito *et al.,* 2002; Ouzounis *et al.,* 1993). For example, guest residues in specific secondary structures have been used as probes of the conformational preference of amino acids, therefore yielding structural conformation data (Patrice and Michael, 1999). Statistical surveys of proteins with known structures revealed that amino acids have clear conformational preferences for one

type of secondary structure (Suyama *et al.,* 1997; Tuckwell *et al.,* 1995; Von *et al.,* 2003). The whole field of secondary structure prediction is concerned with analyzing how these preferences determine whether a sequence segment resides in an α-helix, a β-sheet, or neither. This has led to the development of different methods and models based directly on statistical data, physicochemical properties of amino acids, multilayered neural networks, evolutionary information and multiple sequence alignments.

Previously, patterns of amino acid substitutions in various secondary structure types have been analyzed. For example, Overington *et al*. (1994) constructed amino acid substitution tables for different structural environments defined by sidechain accessibility, hydrogen bonding and secondary structure. Secondary structure-dependent (or more generally, environment-dependent) amino acid substitution tables have been used for fold/domain recognition (Luthy *et al*,., 1991; Johnson *et al*., 1997) and secondary structure predictions (Wako and Blundell, 1994; Mehta *et al*., 1995). Other fold or domain recognition methods have used various types of scoring matrices (Levin *et al.,* 1993; Mugilan and Veluraja, 2000), designed specifically to evaluate matches at each residue between the predicted secondary structure state for the probe and the known or predicted states for the target (Russell and Barton, 1993; Aurora and Rose, 1998). Substitution matrices have been derived to evaluate the degree of match between two structures, or a structure and a sequence. The substitution matrices are calculated from averages over many positions in aligned sequences rather than individual sequence positions (or secondary structure assignments for individual residues). It was demonstrated that the substitution matrices could be used for (1) rapid structure comparisons (e.g. Sequential Structure Alignment Program, Orengo and Taylor, 1990; and comparison of spatial arrangements of secondary structural elements in proteins, Mizuguchi and Go, 1995); and (2) domain recognition (Rice and Eisenberg, 1997).

Modern drug discovery often involves reconstructing and the modeling of small proteins for their ability to bind to molecular targets (Harpreet and Raghava, 2002; Prasad *et al.,* 2003). Target-oriented syntheses of small proteins or a collection of small proteins capable of perturbing a disease-related biological pathway, may eventually lead to the identification of therapeutic molecular targets capable of being modulated by small-reconstructed proteins. One of the ways in which proteins are modified is through site directed mutagenesis. Using site-directed mutagenesis the information in the genetic material can be changed from one particular amino acid code to another (Geourjon and Deleage, 1995). This reprogramming directs the synthesis of a protein with an exchanged amino acid. This method allows us to study in detail how proteins function and how they interact with other biological molecules. Site-directed mutagenesis can be used, for example, to systematically change amino acids in enzymes, in order to better understand the function of these important biocatalysts (Dwyer *et al.,* 2004) and how they fold into their biologically active three-dimensional structures. The method can also be used to study the complex cellular regulation of the genes and to increase our understanding of the mechanism behind genetic and infectious diseases.

Some studies are interested in creating enzymes with new specificities. For example it would be attractive to design an enzyme that can recognize a different substrate and convert it into a valuable product. Generally, single mutations are not expected to have a drastic enough effect as to alter an enzyme's substrate recognition pattern because many amino acid residues in the enzyme (often not close to one another in the primary sequence) affect the binding of the substrate to the enzyme. Obviously, several amino acid residues may need to be altered simultaneously to achieve the goal of changing substrate specificities. Generally, it is unknown which of these combinations will be desirable, as it is difficult to predict, on the basis of a

primary sequence, what the three-dimensional structure of a protein (and of the active site) will be. Introducing essentially all different combinations, which are usually not possible either because of scale or functional constraints, often makes such attempts practically infeasible. Instead, one may choose intelligent design methods; to determine which amino acid substitutions will alter the structure or function of the target protein. Thus the solution to this problem is to develop a method, which would predict the structure of proteins subjected to amino acid substitutions rather then testing thousands of possible combinations. Recently Dwyer, Hellinga and Looger (2004) have demonstrated the viability of this approach where they designed a ribose binding protein to function as triose phosphate isomerase by inducting 18-22 mutations into the ribose-binding protein, a receptor that normally lacks enzyme activity.

There are various methods that predict the structure of a protein, like RPS-BLAST and PSI-PRED which base their predictions on the pre-existing protein structures (Kaur and Raghava 2004). Therefore, these methods may not be the best method to predict the structure of mutated or amino acid substituted proteins where comparative analysis is made based on preexisting protein structures. According to Xuhua and Wen (1998) protein structural predictions based on the amino acid composition of proteins and the pattern of nonsynonymous substitutions perform better in predicting the structure of mutated or substituted proteins. However, their prediction methods use only 134 amino acid properties. Hence the goal of our study was to develop a method to calculate the impact of amino acid substitution on the structural stability of the resultant protein by using 494 amino acid properties.

In 1988 Nakai et al. collected 222 amino acid indices from research papers and investigated the relationship by the hierarchical cluster analysis. They identified four major classes of amino acid properties; α-helix and turn propensities, β-strand propensity, hydrophobicity, and other

physicochemical properties such as comparator and bulkiness of amino acid residues. In 1996, Tomii and Kanehisa increased the size of the collection to include 402 indices and re-performed the clustering. The result was generally in good agreement with the previous work, but for the sake of convenience the collection was divided into six major categories: amino acid composition, hydrophobicity, α-helix and turn propensities, β-strand propensity, physicochemical properties, and other properties. Tomii and Kanehisa (1996) also collected 42 amino acid mutation matrices from the literature and conducted extensive analysis on the correlations among them and with the amino acid indices. The AAindex database was initiated by Nakai et al. (1988), was expanded by Tomii and Kanehisa (1996) and is continuously updated by these authors. (Kanehisa *et al.,* 1999).

Our approach in the present work was to select amino acid property sets whose values were conserved between proteins with similar structure. These property sets, one per amino acid residue, were used to identify amino acid substitutions that shared similar conserved property values. Amino acid profiles were compiled for various levels of conservation and representative amino acids from each profile were substituted into each position of the consensus sequence. The selected sequences were compared to proteins with known conserved domains and three-dimensional structure (RPS-BLAST) and a predicted secondary structure (PSI-PRED). The substituted sequences that matched the original data set sequence were considered to contain substitutions that conserved the structure of the test protein. These amino acid substitutions were found to correlate with a high substitution index value.

Materials and Methods

The computational approach of the present work is briefly illustrated in figure 1. The entire analysis is comprised of different integrated elements including various public domain data base tables such as CCD (Bauer *et al*., 2002) and AAindex (Kanehisa *et al*., 1999) as well as the local database (MySQL Version 4.0.15.). Various freely available resources and procedures, critical for the present analysis were also used for validating this approach (PSI-PRED, http://bioinf.cs.ucl.ac.uk/psipred/psiform.html and RPS-BLAST, http://www.ncbi.nlm.nih.gov/).

Amino acid index (AAindex). AAindex is a database of numerical indices representing various physicochemical and biochemical properties of amino acids and pairs of amino acids. It consists of two sections: AAindex1 is the amino acid index of 20 numerical values for 494 properties and AAindex2 contains the amino acid mutation matrix of 210 numerical values. The database is accessible through the DBGET/LinkDB system at GenomeNet (http://www.genome.ad.jp/dbget/) or may be downloaded by anonymous FTP (ftp://ftp.genome.ad.jp.db/genomenet/aaindex/) (Kanehisa *et al.,* 1998).

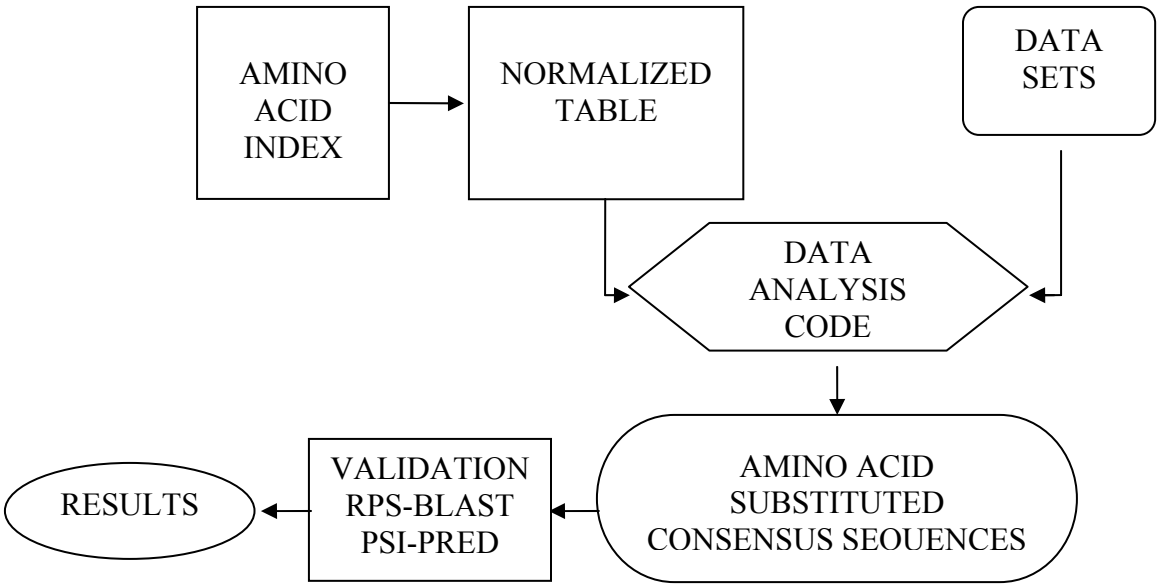

Figure 1. **Diagrammatic overview of the amino acid substitution analysis and validation of the results.** The Amino Acid Index is a stored database table containing 494 published properties for each of the 20 amino acids. The values from this database were normalized for each property so that the Normalized Table contained properties with a mean of zero and a standard deviation of 1, resulting in equally weighted properties. Protein sequences (datasets) from conserved domain database (CCD) with conserved and aligned structures were compiled into 10 Data Sets. The normalized amino acid values were mapped onto the protein sequences from each of the data sets and subjected to the data analysis code to select amino acids substitutions (AA-Profiles). Amino acids from profiles with defined levels of confidence were substituted into a consensus sequence for each of the 10 data sets and their structure compared to a primary dataset sequence during Validation with RPS-BLAST and PSI-PRED. Statistical analysis of the results allowed the selection of the amino acid substitution profile levels that best maintained structure.

The AAindex database is a flat file database that consists of two sections: AAindex1 for the amino acid indices and AAindex2 for the amino acid mutation matrices (Jones *et al.,* 1999). The AAindex1 section currently contains 494 amino acid property indices. Each entry consists of an accession number, a short description of the index, the reference information and 20 numerical values for the property. In addition it contains neighbor information, namely, cross-links to similar indices with an absolute value of the correlation coefficient of >= 0.8 (Shuichi *et al.,* 1999;). The AAindex2 section currently contains 71 AA mutation matrices: 52 symmetric matrices and 19 non-symmetric matrices (Takeshi *et al.,* 1999).

Normalized Table. The property values that were retrieved from the amino acid index database were normalized such that for each property the mean of the 20 amino acid values was set to zero and the standard deviation set to one to avoid weighting bias. These normalized values were stored in a local database (MySQL, version 4.0.15.) in a table called Normalized Table, which has property numbers as the row numbers (001-494) and the 20 amino acids as column headings (Appendix E).

Data Sets

The test data set were obtained from the conserve domain database (CDD) (Aron et al., 2003) hosted by the National Center for Biotechnology Institute (NCBI). Individual data sets (as illustrated in figure 2) comprised of structurally aligned conserved domain sequences (Benner et al., 1994) that were derived from a computational method called VAST (Gibrat *et al*., 1996). The VAST method takes a query protein as input and gives a set of sequences whose aligned domains are structurally conserved. The aligned sequences may have different amino acid sequences

and/or different functions but are all structurally similar with expected value less than or equal to 0.01 (E-value < 0.01) (Stephen *et al.,* 1997). Those sequences towards the top of the alignment are structurally most related to the consensus sequence and to the initial query protein (Tuckwell *et al.,* 1995). The complete sequences for the 10 data sets used in this study may be found in appendix B. These aligned sequences for each data set were further processed to exclude gaps and unaligned regions. According to the Discrete-Space Model (Hidden Markov Model, Stultz *et al*., 1993; Hubbard *et al.,* 1998; Di Francesco *et al*., 1996) excluding the gaps should not have a significant effect on the sequence analysis. A processed sequence fit for the example shown in the figure 2 is found in figure 3. The processed sequences were used as input from a file and the complete listing of the processed data sets can be found in appendix C. The number of sequences in a single data set generally ranged from 7-10. All the sequences in a single processed data set were of same length and are derived from corresponding structural position numbers.

```
            10        20        30        40        50        60
               ....*....|....*....|....*....|....*....|....*....|....*....|
Consensus    1 MIIKPK-VRGFICRTAHPVGCEANVKEQIAYVKKAGKIKNGPKRVLVIGASSGYGLAARI 59
gi 9658208   1 MHIKPI-IQGVVARSAHPYGCEQAVLQQIQYVKQANPIKSGPKRVLILGASSGFGLAARI 59
gi 27358280  1 MRIEPI-IQGVVARSAHPFGCEAAIKKQIAFVKNAPQISQGPKRVLILGASSGFGLAARI 59
gi 28809171  1 MRIEPL-IQGVVARSAHPYGCHASIKEQIEYVKKAPKIKSGPKRVLIIGASSGFGLAARI 59
gi 15981993  1 MIIKPR-VRGFICVTAHPTGCEANVKKQIDYVTTEGPIANGPKRVLVIGASTGYGLAARI 59
gi 24986379  2 AIIHPK-VRGFICTTTHPKGCELNVRDQIEATRKLGVREDGPKKVLVIGASSGYGLAARI 60
gi 28057027 24 LIIHPK-TRGFICTTTHPVGCEYNVLEQIQSTRARGVRSNGPKKVVVIGASSGYGLATRI 82
gi 18145738  1 MIVEPK-FRGFICTTSHPIGCKKNVENQIEYVKENGKI-EGAKRVLVLGASTGYGLASAI 58
gi 15023320  1 MIVKAKfVKGFI-RDVHPYGCRREVLNQIDYCKKAIGF-RGPKKVLIVGASSGFGLATRI 58
```

Figure 2. **Example of a partial Dataset for Alcohol dehydrogenase.** Fragment of the alcohol dehydrogenase data set consisting of the consensus sequence and structurally aligned sequences. These aligned sequences are the search results of the VAST program that are most similar in structure to query protein (gi 9658208). The gi 9658208 sequence is called the VAST query sequence for this data set. The number of sequences selected by VAST depends on how significant these matches are to the query protein (significant, E-value <= 0.001). The consensus sequence contains the most common amino acids among the aligned sequences. The lowercase letters represent regions that are not structurally conserved whereas the upper case letters are structurally conserved regions. Note that it was not conditional for these aligned sequences to have a similar function. The processed input file sequences (figure 3) show only the uppercase amino acid letters corresponding to the structurally conserved domains. The gaps and lower case letters excluded from the input file are found in Appendix: C.

```
Consensus       MIIKPKVRGFIRTAHPVGCENVKQIAYVKGKIGPKRVLVIGASSGYGLAARI
gi 9658208      MHIKPIIQGVVRSAHPYGCEAVLQIQYVKNPIGPKRVLILGASSGFGLAARI
gi 27358280     MRIEPIIQGVVRSAHPFGCEAIKQIAFVKPQIGPKRVLILGASSGFGLAARI
gi 28809171     MRIEPLIQGVVRSAHPYGCHSIKQIEYVKPKIGPKRVLIIGASSGFGLAARI
gi 15981993     MIIKPRVRGFIVTAHPTGCENVKQIDYVTGPIGPKRVLVIGASTGYGLAARI
gi 24986379     AIIHPKVRGFITTTHPKGCENVRQIEATRGVRPPKKVLVIGASSGYGLAARI
gi 28057027     LIIHPKTRGFITTTHPVGCENVLQIQSTRGVRGPKKVVVIGASSGYGLATRI
gi 18145738     MIVEPKFRGFITTSHPIGCKNVEQIEYVKGKIGAKRVLVLGASTGYGLASAI
gi 15023320     MIVKAKVKGFIRDVHPYGCREVLQIDYCKIGFGPKKVLIVGASSGFGLATRI
```

Figure 3. **Alignment of processed sequences from alcohol dehydrogenase.** Example of the output sequence generated by processing the sequences in figure 2 where the gaps and lower case letters have been removed.

Algorithm

The algorithm for the analysis was written in Perl (Programming language, Version 5.8). The entire program (Appendix: A) is subdivided into various functions, which perform specific computational tasks as outlined in figure 4 and in figure 5-7.

Input sequence processing. The sequences in each data set were processed to remove gaps and regions which were non-conserved. The initial data set sequences can be found in appendix B and an example is shown in the figure 2 with the gaps and lower case letters representing amino acids that are not structurally aligned. The final sequences as shown in figures 3 and Appendix C represent only those regions, which were structurally conserved between all the sequences in the dataset.

Difference Values. Pair-wise couplets were created for all possible combinations of the aligned sequences (figure 5b). A vector of property values developed from the normalized table were mapped onto the amino acids in the couplets (figure 5c, d and e). Property difference vectors were calculated by taking the absolute value of the difference between the two property vectors from each of the couplets (figure 5e). Properties within the difference vector with values less than or equal to difference critical value were saved into the property index pool (PIP) (figure 5f).

A difference of one was used as the difference critical value for our analysis (figure 5f) because it offered a trade off between Type I and Type II errors and was found to function with consistent results.

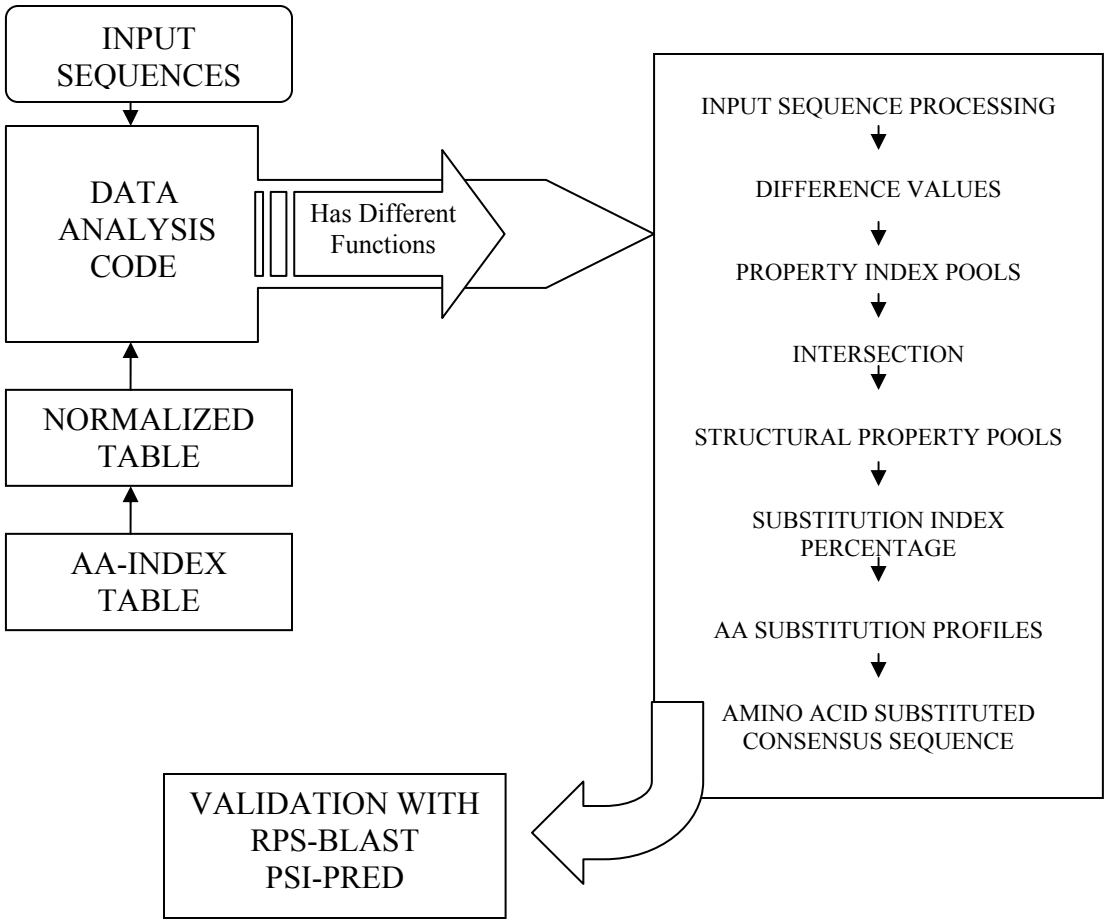

Figure 4. **Overview of the computational flow of the processing program.** This diagrammatic representation shows different functions (Subroutines) in the data analysis part of the code. The first function takes the input sequences, process them to remove gaps and unaligned regions, and pass them to the next function and so on until amino acid substituted consensus sequences are generated by the last function. These substituted sequences are then processed by RPS-BLAST and PSI-PRED, to determine if structure remains the same as for un-substituted sequences. Detailed description on these functions follows in the later sections.

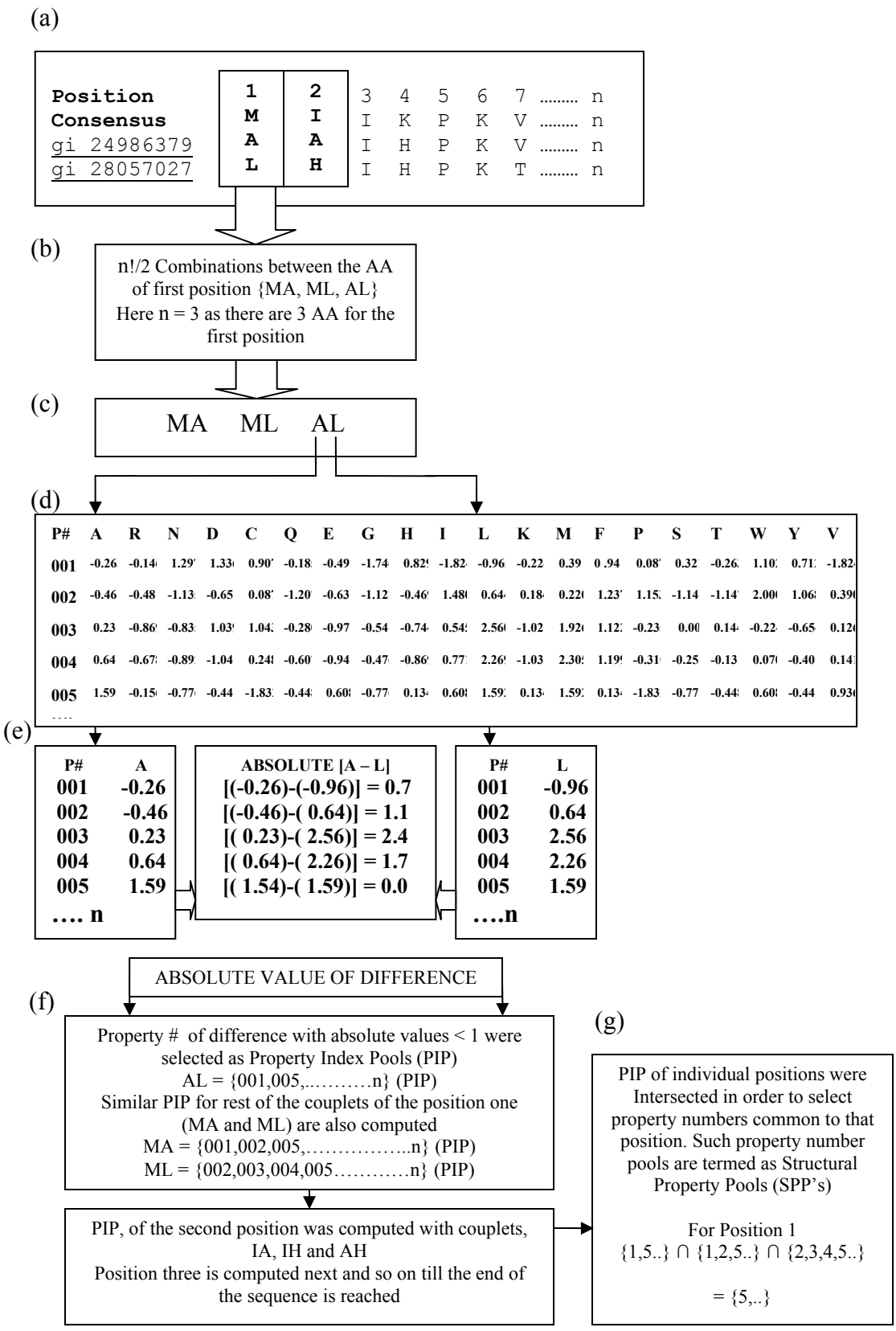
(a)
Position
Consensus
gi 24986379
gi 28057027
1 M A L
2 I A H
3 4 5 6 7 ..... n
I K P K V ..... n
I H P K V ..... n
I H P K T ..... n
(b)
n!/2 Combinations between the AA of first position {MA, ML, AL}
Here n = 3 as there are 3 AA for the first position
(c)
MA ML AL
(d)
P# A R N D C Q E G H I L K M F P S T W Y V
001 -0.26 -0.14 1.29 1.33 0.90 -0.18 -0.49 -1.74 0.82 -1.82 -0.96 -0.22 0.39 0.94 0.08 0.32 -0.26 1.10 0.71 -1.82
002 -0.46 -0.48 -1.13 -0.65 0.08 -1.20 -0.63 -1.12 -0.46 1.48 0.64 0.18 0.22 1.23 1.15 -1.14 -1.14 2.00 1.06 0.39
003 0.23 -0.86 -0.83 1.03 1.04 -0.28 -0.97 -0.54 -0.74 0.54 2.56 -1.02 1.92 1.12 -0.23 0.00 0.14 -0.22 -0.65 0.12
004 0.64 -0.67 -0.89 -1.04 0.24 -0.60 -0.94 -0.47 -0.86 0.77 2.26 -1.03 2.30 1.19 -0.31 -0.25 -0.13 0.07 -0.40 0.14
005 1.59 -0.15 -0.77 -0.44 -1.83 -0.44 0.60 -0.77 0.13 0.60 1.59 0.13 1.59 0.13 -1.83 -0.77 -0.44 0.60 -0.44 0.93
....
(e)
P# A
001 -0.26
002 -0.46
003 0.23
004 0.64
005 1.59
…. n
ABSOLUTE [A – L]
[(-0.26)-(-0.96)] = 0.7
[(-0.46)-(0.64)] = 1.1
[(0.23)-(2.56)] = 2.4
[(0.64)-(2.26)] = 1.7
[(1.54)-(1.59)] = 0.0
P# L
001 -0.96
002 0.64
003 2.56
004 2.26
005 1.59
….n
ABSOLUTE VALUE OF DIFFERENCE
(f)
Property # of difference with absolute values < 1 were selected as Property Index Pools (PIP)
AL = {001,005,..……n} (PIP)
Similar PIP for rest of the couplets of the position one (MA and ML) are also computed
MA = {001,002,005,……..n} (PIP)
ML = {002,003,004,005……n} (PIP)
PIP, of the second position was computed with couplets, IA, IH and AH
Position three is computed next and so on till the end of the sequence is reached
(g)
PIP of individual positions were Intersected in order to select property numbers common to that position. Such property number pools are termed as Structural Property Pools (SPP's)
For Position 1
{1,5..} ∩ {1,2,5..} ∩ {2,3,4,5..}
= {5,..}

Figure 5. **Example of difference value processing for three alcohol dehydrogenase sequences.** (a) Fragment of the Alcohol Dehydrogenase, structural alignment which is equivalent to the processed sequence found in Appendix C. Highlighted amino acids enclosed in a box belong to the position one and two. (b) n!/2 combinations were generated for each individual position, in order to compare all the sequences. (c) Combination Pool showing three couplets resulting from combinations in position one. (d) Normalized table which holds the property values for each amino acid (column) and property (row) combinations (e) Property values of a couplet were subtracted from each other (AL) and then converted to an absolute value. (f) Property Numbers with resultant absolute values less than one were selected to be in the Property Index Pool (PIP). PIP's were then generated for all combinations at each position along the sequence. (g) At each position properties that were common to all PIP's become members of the Structural Property Pool (SPP).

Abbreviations used were 'n', which stands for the number of aligned sequences, AA is amino acid and # represents number.

Property Index Pools (PIP). PIP comprises the property numbers of the properties with differences that have an absolute value less than one (figure 5f). The total number of PIP sets generated for a single position is equal to the total number of couplets generated from the combination (n!/2). From the example in the figure 5f, the PIP's generated for the first position were AL = {001,005,..……n}, MA = {001,002,005,……..n} and ML = {002,003,004, 005……n} where the value of 'n' ranged up to 494.

Intersection. Properties that were common to all PIP's for a position represent a conserved property important to the structure of the protein. An intersection between the PIP sets, as seen in figure 5g, selected property numbers common to all of the PIP's of that position (figure 6). These selected property numbers were called the Structural Property Pools (SPPs).

Structural Property Pools. SPPs were composed of the conserved properties from PIPs. There is one SPP for each position in data set.

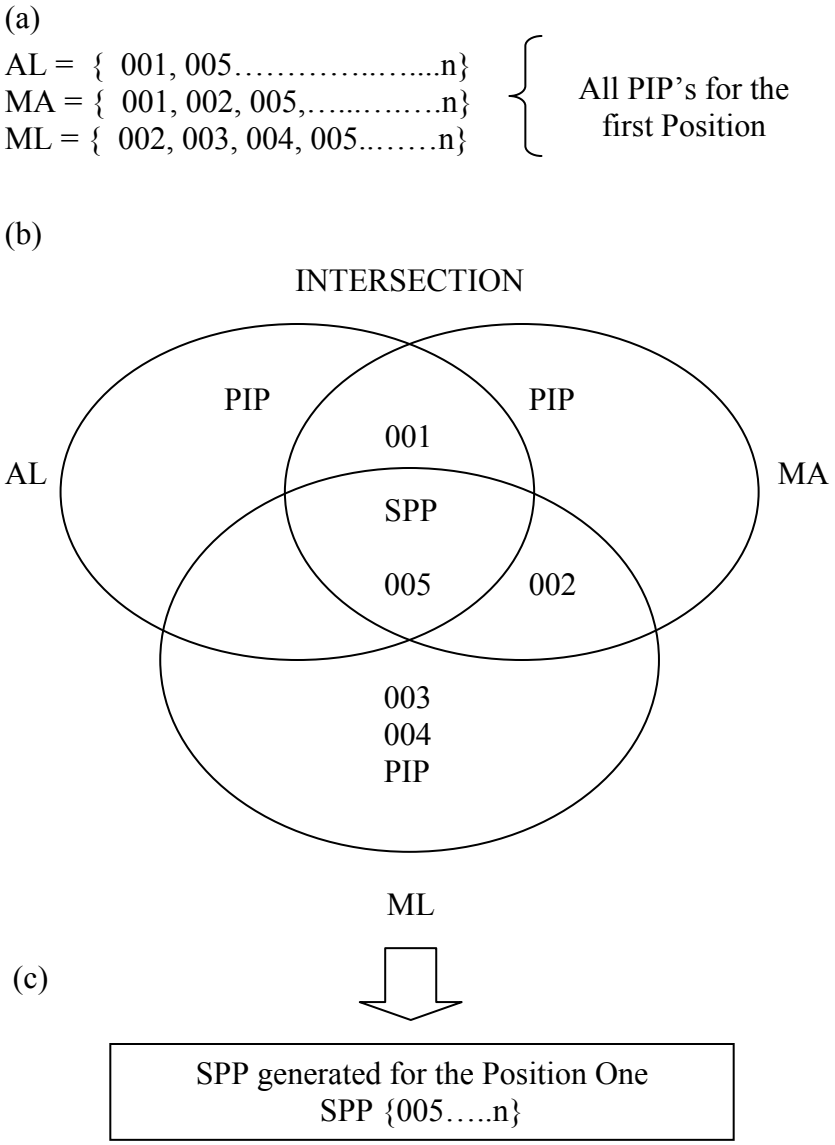

Figure 6. **SPP selected from intersection of PIP property sets.** (a) PIP's for the first position demonstrated in figure 5, showing the selected property numbers. (b) Intersection between the PIP sets from the three couplets for the first position. (c) SPP for the first position showing one conserved property with property number 005.

Substitution Index Percentage (SI%). Substitution index percentage was a numerical representation of the extent to which one amino acid can be substituted in the place of another amino acid at a particular position. A stepwise illustration of the computational procedure associated with this function is demonstrated in figure 7.

Amino Acid Substitution Profiles (AASP). Amino acid substitution profiles were a set of amino acids profiles at each sequence position that have SI% within a defined range. In order to define an acceptable range of SI% that would identify substitutions that would conserve structure, we selected three SI% ranges of profiles: α (90% <= SI% <= 100%), β (80% <= SI% < 90%) and γ (70% <= SI% <80%).

Amino Acid Substituted Consensus Sequence (AASCS). Amino acid substituted consensus sequences (AASCS) were generated by substituting amino acids from the profile ranges, defined by AASP, into the consensus sequence for a corresponding data set. One AASCS was generated from each SI% profile range in the 10 data sets. The AASCS for each data set can be found in Appendix D. Amino acids with the highest SI% within each category were selected for substitution. Because individual profile categories had variable numbers of amino acid SI% within each range, only amino acids with the highest SI% were selected. Faster computational resources were needed to test all the possible substitutions.

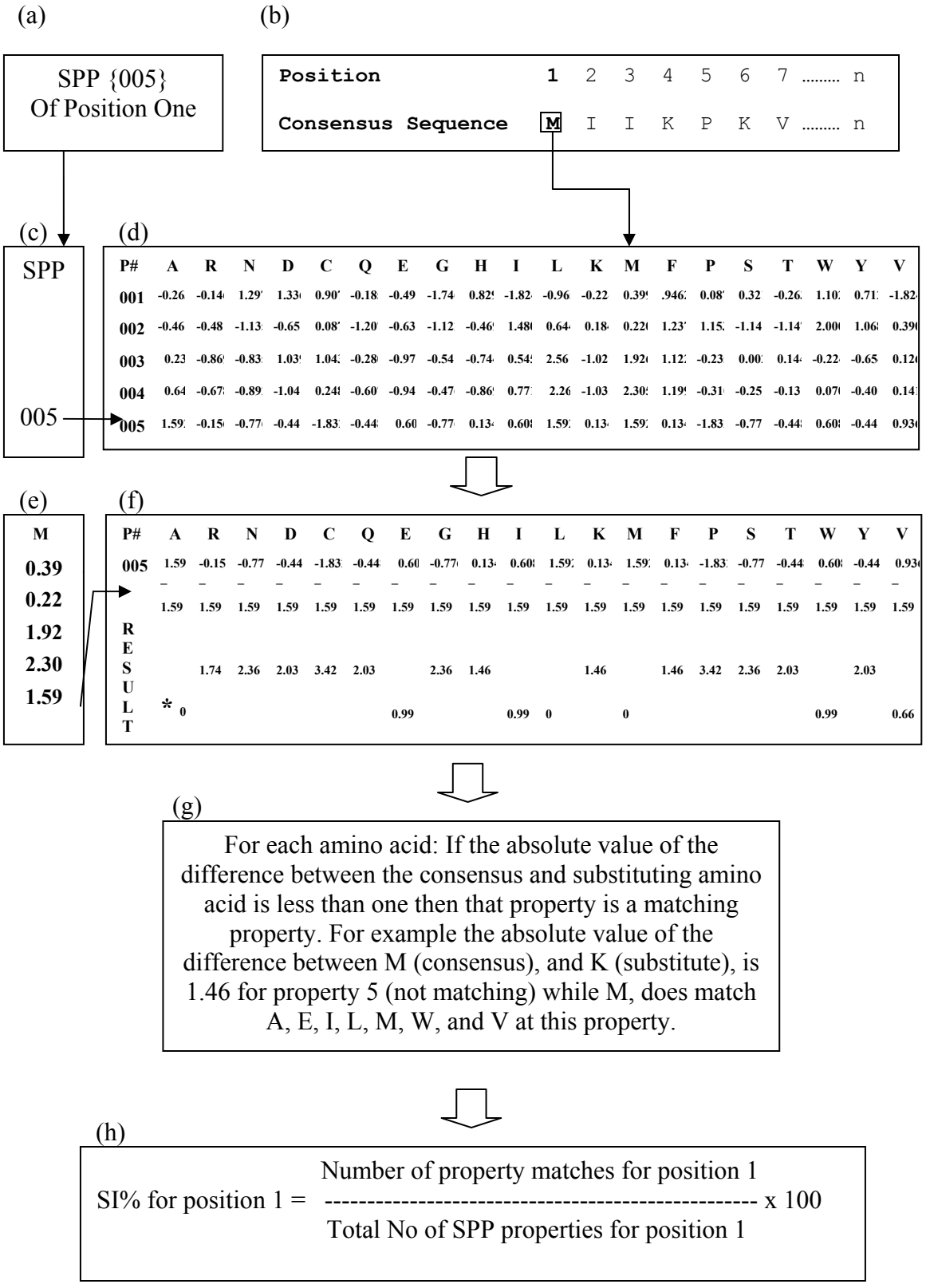
(a)
SPP {005}
Of Position One
(b)
Position 1 2 3 4 5 6 7 ..... n
Consensus Sequence M I I K P K V ..... n
(c)
SPP
005
(d)
P# A R N D C Q E G H I L K M F P S T W Y V
001 -0.26 -0.14 1.29 1.33 0.90 -0.18 -0.49 -1.74 0.82 -1.82 -0.96 -0.22 0.39 .946 0.08 0.32 -0.26 1.10 0.71 -1.82
002 -0.46 -0.48 -1.13 -0.65 0.08 -1.20 -0.63 -1.12 -0.46 1.48 0.64 0.18 0.22 1.23 1.15 -1.14 -1.14 2.00 1.06 0.39
003 0.23 -0.86 -0.83 1.03 1.04 -0.28 -0.97 -0.54 -0.74 0.54 2.56 -1.02 1.92 1.12 -0.23 0.00 0.14 -0.22 -0.65 0.12
004 0.64 -0.67 -0.89 -1.04 0.24 -0.60 -0.94 -0.47 -0.86 0.77 2.26 -1.03 2.30 1.19 -0.31 -0.25 -0.13 0.07 -0.40 0.14
005 1.59 -0.15 -0.77 -0.44 -1.83 -0.44 0.60 -0.77 0.13 0.60 1.59 0.13 1.59 0.13 -1.83 -0.77 -0.44 0.60 -0.44 0.93
(e)
M
0.39
0.22
1.92
2.30
1.59
(f)
P# A R N D C Q E G H I L K M F P S T W Y V
005 1.59 -0.15 -0.77 -0.44 -1.83 -0.44 0.60 -0.77 0.13 0.60 1.59 0.13 1.59 0.13 -1.83 -0.77 -0.44 0.60 -0.44 0.93
– – – – – – – – – – – – – – – – – – – –
1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59 1.59
RESULT
1.74 2.36 2.03 3.42 2.03 2.36 1.46 1.46 1.46 3.42 2.36 2.03 2.03
* 0 0.99 0.99 0 0 0.99 0.66
(g)
For each amino acid: If the absolute value of the difference between the consensus and substituting amino acid is less than one then that property is a matching property. For example the absolute value of the difference between M (consensus), and K (substitute), is 1.46 for property 5 (not matching) while M, does match A, E, I, L, M, W, and V at this property.
(h)
SI% for position 1 = Number of property matches for position 1 / Total No of SPP properties for position 1 x 100

Figure 7. **Using SPP to calculate SI% for each amino acid substitution from the alcohol dehydrogenase example in figure 6.** (a) The SPP for position 1 included property #005 (figure 5g and figure 6). (b) The consensus sequence for the first position of the alcohol dehydrogenase was M (Methionine). (c) Properties in the SPP were located in the Normalized Table (d). (e) Values for the consensus amino acids were selected and subtracted from each of the corresponding property values for the 20 amino acids (f) The absolute value of the property difference were calculated and recorded as results (f). Those results in the * row were less than 1 and considered to be matched properties (fg). (h) The SI% for an individual substituted amino acid is calculated by adding the number of matching properties divided by the total number of SPP properties multiplied by 100. This generates 20 SI% values for each position. The SI% gives a relative weight of conservation for substitution by each of the twenty amino acids at a given position in the consensus sequence.

Validation of Structure Conservation. In order to confirm that substituted consensus sequences (AASCS) would maintain their structure, secondary structures for each of the AASCS sequences was predicted with the PSI-PRED (Position Specific Iterated Prediction) program and compared to the VAST-query sequence (example shown in figure 2). A second comparison was made by RPS-BLAST (Reverse Position-Specific BLAST) which matches sequences to conserved domains, including known conserved 3D domains; again, an AASCS match to the VAST-query sequence (example shown in figure 2) was given positive score. Similar analyses were done on the consensus sequence for each dataset.

The RPS-BLAST Reverse Position-Specific BLAST program can be used to identify conserved domains in protein sequences. Thus, it was used to retrieve domain alignments including 3D structures. RPS-BLAST takes a protein sequence as input and returns a set of significant matches (E-Value <= 0.01) based on conserved structure (Marchler *et al*., 1999). However, the level of stringency in this analysis was increased to E-Value <= 0.001 (Igor and Sung, 1999). A positive match was identified if the VAST query sequence was returned and negative match if the VAST query sequence did not fall with in the significant E-value.

PSI-PRED predicts the secondary structure of a protein with accuracy greater than 82%. This program takes an input sequence and, based on the neural net algorithms, generates a hypothetical secondary structure which is used to search the PDB database for similar matches. The program returns the best pairwise matched sequence to the input sequence. PSI-PRED is a simple and reliable secondary structure prediction method, incorporating two feed-forward neural networks, which perform an analysis on output obtained from (protein-protein BLAST) PSI-BLAST (Yang and Wang, 2002). PSI-BLAST return significant matches (E <=0.001) to the neural net of PSI-PRED. Among these matches the best match is selected by the neural network

of the PSI-PRED. PSI-PRED includes a new algorithm which averages the output from up to 4 separate neural networks in the prediction process to further increase prediction accuracy (Burkhard and Chris, 1993). This program was used to further validate the results from RPS-BLAST.

Random sequences. Taking the consensus sequences and randomizing the position of the amino acids without altering the composition of the protein sequence generated random sequences. The resulting sequences were then fed into PSI-PRED and RPS-BLAST as a negative control to test the sensitivity of these programs to random sequence disruption.

Statistical Analysis

Because the output of the PSI-PRED and RPS-BLAST comparisons had only two possible outcomes, match or non-match, we used one tailed Binomial probability tests to determine the significance of the numbers of matches vs. non-matches within each SI% category α, β, γ. We also used pair-wise binomial probability tests to compare relationship between α-AASCS, β-AASCS, γ-AASCS, consensus sequences and randomized sequences. Finally, this same test was used to compare the outputs of the PSI-PRED and RPS-BLAST methods.

Binomial Probability Test. If matches between two sequences were truly random then the probability used in the binomial distribution that describes a sampled group of such matches would be 0.5 (i.e., equal probability of getting a match or a non-match). If the value for the type I error limit is set to 0.05 then sampled groups, with upper tail probability of $P = 1\text{-CDF} < 0.05$. Therefore, this would infer that there is a significant non-random relationship between the sampled groups.

When there were 8, 9, or 10 matches out of the ten datasets then these matches were considered very significant (table 1) and implied that there was a positive relationship between the AASCS and the VAST query sequence.

Two SI% categories of datasets were similarly tested against each other or against the consensus or randomized sequence categories. To do this matches were defined by comparing the + or – values between corresponding datasets from two categories. Datasets that had both positive (+,+) or both negative (-,-) relationships were considered matches (+). Data sets that show (+,-) or (-,+) relationship were considered non-matches (-). The resultant data set matching values were evaluated for significant non-random relationships by using the binomial probability distribution as seen in the table 1. Similarly, comparisons were made between datasets from RPS-BLAST and PSI-PRED to test the significance of the relationship between the two validation methods.

Calculations were carried out using Bonferroni adjustment of 0.05/n where n=3 tests yielded similar results hence only the former are reported.

Table 1.**Binomial Probability Table.** Shows the probability density function values for the number of matches ranging from zero to ten for the 10 trials. The probability of getting a match was set to 0.5 for the probability density function (center column). The distribution suggests that getting five successes out of 10 has higher probability than getting zero or one. The Left column represents the number of successes in a trial of ten and the right column represents the upper tail of the binomial distribution and is computed by subtracting cumulative density function (lower tail) from 1.

Number of matches out of 10 datasets	**Probability Density Function values for each match**	**Upper tail probability, P, where P=1-CDF (Cumulative Density Function)**
0	0.0010	0.9990
1	0.0098	0.9892
2	0.0439	0.9453
3	0.1172	0.8281
4	0.2051	0.6230
5	0.2461	0.3770
6	0.2051	0.1719
7	0.1172	0.0547
8	0.0439	0.0107
9	0.0098	0.0010
10	0.0010	0.0000

Results and Discussion

The goal of our study was to develop a method that would predict amino acid substitutions that could be placed in a protein while still maintaining the structural organization of the resultant protein.

Starting with 10 datasets, each with 7-8 proteins, we selected conserved structural domains that matched a query protein in a VAST alignment. From the alignment sequence we calculated substitution indexes (SI%) for each amino acid at each position in each dataset. Amino acid substitution profiles were compiled for three SI% ranges: α (90% <= SI% <=100%), β (80% <= SI% < 90%) and γ (70% <= SI% < 80%). These profiles were used to make substitutions into the consensus sequence of each of the datasets resulting in amino acid substituted consensus sequences (AASCS).

Our hypothesis was that the greater the substitution index percentage the greater the similarity or conservation of the protein structure, and that AASCS from the three percentage ranges would not all equally match the consensus sequence in their corresponding data set. If true, then only a few amino acids could be effectively substituted into the consensus sequence.

Our AASCS were compared to structural databases using programs, RPS-BLAST and PSI PRED. The AASCS that showed significant matches to their respective data set VAST query sequences were positively scored. The results were used to test the hypothesis that the AASCS were significantly related to the VAST query sequence, using the Binomial Probability Test (The detailed procedure is provided in the materials and methods section). A number of positive scores were compared to a binomial distribution and the probability that the positive matches

were observed at random was determined for each SI% range and also for consensus and randomized sequences.

α-AASCS (SI% range 90-100%) compared to the VAST query sequence and the Consensus Sequence. The consensus sequence served as a positive control in our study. A 100% match of the consensus sequences to the VAST-query sequences by RPS-BLAST and PSI-PRED (Tables 2a, 3a, 4a, 5a) suggested that the consensus sequence were significantly similar to the VAST query sequences hence, the consensus sequence was used for creating AASCS substitutons. The results from RPS-BLAST and PSI-PRED for the 'α' SI% category showed a significant positive relationship between the α-AASCS and both the VAST-query sequence and also to the consensus sequence (P<0.01) (Table 2a and 2b respectively). There was a low probability of finding these pattern matches at random suggesting that there is a significant relationship between the α-AASCS and the consensus (the unsubstituted form of AASCS). These data also suggest that amino acid substitutions from the 'α' category conserve the protein structure.

β-AASCS (SI% range 80-89%) compared to the VAST query sequence and the Consensus Sequence. Results of RPS-BLAST and PSI-PRED showed no significant positive relationship between the β-AASCS to either the VAST-query sequence nor to the consensus sequence (P = 0.18) (table 3a and 3b respectively). There is a high probability that this resultant pattern could be obtained by random sampling. These results suggest that β-AASCS's are not significantly similar to the consensus sequences and that the amino acid substitutions from this category could significantly alter the structure of the protein.

γ-AASCS (SI% range 70-89%) compared to the VAST query sequence and the Consensus Sequence. The results from RPS-BLAST and PSI-PRED for the 'γ' SI% category AASCS showed no significant positive relationship (P>0.05) between the γ-AASCS and both the VAST-query sequences and the consensus sequences (table 4a and 4b respectively). The comparison suggests that the amino acids within the 'γ' category will significantly alter the structure of the protein.

Random Sequence Compared with Consensus Sequence. It is known that the amino acid composition of a protein is critically important in maintaining the structure of the protein because certain regions in proteins rarely change and are conserved over a very long periods of time (Bateman, 1997). Therefore, randomization of the position of the amino acids within the consensus sequences allowed for the creation of negative controls. The results from submitting the random sequence to the RPS-BLAST and PSI-PRED program confirmed the effectiveness of random sequence as a negative control. The completely opposite matches between the random and consensus sequence showed no significant positive relationship between both categories (P=1) (table 5). This inverse relationship suggests that RPS-BLAST and PSI-PRED are effective in discriminating the effect of composition and position of the amino acids within protein sequence. A negative match to the consensus sequence suggests that the position of these amino acids in the protein maybe critical for the maintenances structural conformation.

SI% Category Comparisons. For both the RPS-BLAST and PSI-PRED the 'α' SI% category shows a significant positive relationship between the AASCS and both the VAST-query sequence and the consensus sequence (P<0.01) (table 2). The 'β' SI% category AASCS do not show a significant relationship to either the VAST-query sequences nor to the consensus

sequences ($P = 0.18$) (table 3). The 'γ' SI% category AASCS show no significant relationship to the VAST-query sequences nor to the consensus sequences ($P>=0.95$) (table 4). These data would predict that the α, β and γ SI% AASCS are not significantly related. These predictions were confirmed in the direct pair-wise comparison of these categories for RPS-BLAST and PSI-PRED results both individually and combined (table 6b).

RPS-BLAST support of PSI-PRED results. RPS-BLAST results for the three SI% categories 'α', 'β' and 'γ' are shown in table 6 along with PSI-PRED results from these same categories. There was a high degree of match between the results from the two tests where 26 out of 30 scores matched (table 6a) giving a binomial probability, P, approximately equal to zero. This implies that RPS-BLAST and PSI-PRED results are highly correlated at all of the SI% categories.

Table 2. **Comparison of RPS-BLAST and PSI-PRED results for α-AASCS and the consensus sequences.** (a) RPS-BLAST and PSI-PRED comparisons of α-AASCS and consensus sequences to the VAST query sequences. A significant match was scored as '+' otherwise it was given a '-'. The probability that the number of positive matches within each column of datasets occurred at random is given by P, the upper tail of the binomial probability distribution. (b) The AASCS and consensus sequence patterns were compared by assigning +,+ and -,- patterns as matches and +,- and -,+ patterns as non-matches for each dataset. P, is the probability that the patterns of the two columns positively match at random (Binomial distribution).

(a)

Protein Name	RPS-BLAST Match to α-AASCS	PSI-PRED Match to α-AASCS	RPS-BLAST/PSI-PRED Consensus Match
Ascorbate Peroxidase	+	+	+
Cytochrome-Oxidase	+	+	+
Glucokinase	+	+	+
Glyceraldehyde-3-phosphate Dehydrogenase	-	+	+
Glycerol Kinase	+	+	+
Alcohol Dehydrogenase	+	+	+
Lactate Dehydrogenase	+	+	+
Plant Peroxidase	+	+	+
Succinate Dehydrogenase	+	+	+
Thymidylate Kinase	+	+	+
Probability (P) =	**0.001**	**0**	**0**

(b)

AASCS vs Consensus Sequence	Probability, (P)
RPS-BLAST	0.001
PSI-PRED	0

Table 3. **Comparison of RPS-BLAST and PSI-PRED results for β-AASCS and consensus sequences.** (a) RPS-BLAST and PSI-PRED comparisons of β-AASCS and consensus sequences to the VAST query sequences. A significant match was scored as '+' otherwise it was given a '-'. The probability that the number of positive matches within each column of datasets occurred at random is given by P, the upper tail binomial of the probability distribution. (b) The AASCS and consensus sequence patterns were compared by assigning +,+ and -,- patterns as matches and +,- and -,+ patterns as non-matches for each dataset. P, is the probability that the patterns of the two columns positively match at random (Binomial distribution).

(a)

Protein Name	**RPS-BLAST Match for 'β'**	**PSI-PRED Match for 'β'**	**RPS-BLAST / PSI-PRED Consensus Match**
Ascorbate Peroxidase	+	+	+
Cytochrome-Oxidase	+	+	+
Glucokinase	-	-	+
Glyceraldehyde-3-phosphate Dehydrogenase	+	-	+
Glycerol Kinase	+	+	+
Alcohol Dehydrogenase	-	+	+
Lactate Dehydrogenase	+	+	+
Plant Peroxidase	-	-	+
Succinate Dehydrogenase	-	-	+
Thymidylate Kinase	+	+	+
Probability, (P) =	**0.18**	**0.18**	**0**

(b)

AASCS vs Consensus Sequence	**Probability, (P)**
RPS-BLAST	0.18
PSI-PRED	0.18

Table 4. **Comparison of RPS-BLAST and PSI-PRED results for γ-AASCS and consensus sequences.** (a) RPS-BLAST and PSI-PRED comparisons of γ-AASCS and consensus sequences to the VAST query sequences. A significant match was scored as '+' otherwise it was given a '-'. The probability of that the number positive matches within each column of datasets occurred at random is given by P, the upper tail of the binomial probability distribution. (b) The AASCS and consensus sequence patterns were compared by assigning +,+ and -,- patterns as matches and +,- and -,+ patterns as non-matches for each dataset. P, is the probability that the patterns of the two columns positively match at random (Binomial distribution).

(a)

Protein Name	**RPS-BLAST Match for 'γ'**	**PSI-PRED Match for 'γ'**	**RPS-BLAST/ PSI-PRED Consensus Match**
Ascorbate Peroxidase	+	-	+
Cytochrome-Oxidase	-	-	+
Glucokinase	-	-	+
Glyceraldehyde-3-phosphate Dehydrogenase	-	-	+
Glycerol Kinase	+	+	+
Alcohol Dehydrogenase	-	-	+
Lactate Dehydrogenase	-	-	+
Plant Peroxidase	-	-	+
Succinate Dehydrogenase	-	-	+
Thymidylate Kinase	-	-	+
Probability, (P) =	**0.95**	**0.99**	**0**

(b)

AASCS vs Consensus Sequence	**Probability, (P)**
RPS-BLAST	0.95
PSI-PRED	0.99

Table 5. **Comparison of RPS-BLAST and PSI-PRED results for the randomized and consensus sequences.** (a) RPS-BLAST and PSI-PRED comparisons of random sequences and consensus sequences to the VAST query sequences. A significant match was scored as '+' otherwise it was given a '-'. The probability of that the number of positive matches within each column of datasets occurred at random is given by P, the upper tail of the binomial probability distribution. (b) The AASCS and consensus sequence patterns were compared by assigning +,+ and -,- patterns as matches and +,- and -,+ patterns as non-matches. P, is the probability that the patterns of the two columns match at random (Binomial distribution).

(a)

Protein Name	**RPS-BLAST Random Match**	**PSI-PRED Random Match**	**RPS-BLAST/ PSI-PRED Consensus Match**
Ascorbate Peroxidase	-	-	+
Cytochrome-Oxidase	-	-	+
Glucokinase	-	-	+
Glyceraldehyde-3-phosphate Dehydrogenase	-	-	+
Glycerol Kinase	-	-	+
Alcohol Dehydrogenase	-	-	+
Lactate Dehydrogenase	-	-	+
Plant Peroxidase	-	-	+
Succinate Dehydrogenase	-	-	+
Thymidylate Kinase	-	-	+
Probability, (P) =	**1**	**1**	**0**

(b)

AASCS vs Consensus Sequence	**Probability, (P)**
RPS-BLAST	1
PSI-PRED	1

Table 6. **Comparison of RPS-BLAST and PSI-PRED results for α, β and γ SI% categories.** (a) The results (+ and -) are taken from tables 3, 4 and 5. (b) The corresponding sequence patterns between RPS-BLAST and PSI-PRED were compared where +,+ and -,- patterns were considered to be matches and +,- and -,+ patterns were non-matches. The category comparisons were statistically evaluated using a Binomial probability distribution (table 1). P, is upper tail probability which is equivalent to the Type I error probability. (C) The sequence patterns between RPS-BLAST and PSI-PRED were compared, 'α' with 'α', 'β' with 'β' and 'γ' with 'γ' as described in (b). The upper tail probability that these patterns match at random is expressed as P.

(a)

Protein Name	**RPS-BLAST Match**			**PSI-PRED Match**		
	α	**β**	**γ**	**α**	**β**	**γ**
Ascorbate Peroxidase	+	+	+	+	+	-
Cytochrome-Oxidase	+	+	-	+	+	-
Glucokinase	+	-	-	+	-	-
Glyceraldehyde-3-Phosphate Dehydrogenase	-	+	-	+	-	-
Glycerol Kinase	+	+	+	+	+	+
Alcohol Dehydrogenase	+	-	-	+	+	-
Lactate Dehydrogenase	+	+	-	+	+	-
Plant Peroxidase	+	-	-	+	-	-
Succinate Dehydrogenase	+	-	-	+	-	-
Thymidylate Kinase	+	+	-	+	+	-

(b)

SI% Category Comparisons	**'α' vs 'β'**	**'β' vs 'γ'**	**'α' vs 'γ'**
RPS-BLAST	P = 0.317	P = 0.172	P = 0.828
PSI-PRED	P = 0.172	P = 0.377	P = 0.989
RPS-BLAST + PSI-PRED	P = 0.252	P = 0.252	P = 0.994

(c) RPS-BLAST vs PSI-PRED, P = 0

Conclusions and Implications

The present study was undertaken in order to address the influence various conserved amino acid properties on the structure of proteins. Primary focus was to derive a method through which a controlled selection and substitution of amino acids into a protein could be made possible. The knowledge of precise amino acid selection would in turn make it possible to control the protein structure (Hu *et al.,* 1997; Jens *et al.,* 2003). The knowledge of being able to accurately predict the structure of substituted proteins is very valuable for various areas such as mutational studies, protein engineering, protein designing and drug development etc.

RPS-BLAST and PSI-BLAST identified each consensus sequence as significantly related to its VAST-query sequence (table 2a, 3a, 4a, 5a respectively). The consensus sequences were therefore valid sequences into which substitutions could be placed to test the affect of the substitution on protein structure. Since a change in the position of an amino acid within a protein sequence almost always results in a change in structure (Patrice *et al.,* 1999), randomization of the consensus sequences was used as negative controls to test whether the PSI-PRED and RPS-BLAST programs were sensitive to such rearrangements. Table 5 indicates that they were.

PSI-PRED and RPS-BLAST are two different approaches to the identification of significant matches in structure. The strong identity of matches between them when screening the consensus and random sequences indicate that they are good validation tools for our program (table 5). There is a high degree of match between the results from the two tests with 26 out of 30 scores matching (table 6a) giving a binomial probability (P) approximately equal to zero. This implies that RPS-BLAST and PSI-PRED results are highly correlated at all of the SI% categories.

The three SI% categories, selected to create AASCS, covered the whole spectrum of the binomial distribution. For example there was a significant positive relationship for 'α' in the upper tail of the binomial distribution and a non-significant relationship for 'γ'. The conclusions can be drawn that amino acid substitutions made into consensus sequences from amino acids with SI% ≥ 90% are predicted to maintain the structure of the consensus sequence whereas amino acid substitutions with SI% less than 90% disrupted the structure of the consensus sequence.

These predictions can be used in directing protein engineering. This method makes predictions of amino acid substitutions that not only conserve structure but that also disrupt or change the protein structure.

These prediction data can be very useful in searching for related conserved structures, since a profile of valid substitutions can be generated for each position of the consensus sequence. There are search programs available in the public domain that accepts amino acid profiles like FAST (flexible Analysis by Software Tools) and CHAMP (CHemico-physical AMinoacidic Parameter data bank) which are packages designed to study protein structure by drawing profiles of specific amino acid parameters (Facchiano *et al.,* 1989). Our future studies will focus on generating amino acid profiles for larger datasets. We will also search for sequences using profile searching method and compare matches that have associated structural data to the VAST-query sequences. If generation and searching with profiles proves to be successful then it would provide another rapid method to search for structural relationships.

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APPENDIX

APPENDIX A: PROGRAM

```
#================================================================
# Name                  : Avinash M. Baktula
# Program Description: The program implements a function which process the mFAST
#                       file to remove the gaps the small letters and only
#                       considers the conserved domains and sends the out to a
#                       file after processing.
#================================================================
#!usr/local/bin/perl -w
use strict;
my $count1 = 0; my $count2 = 0; my $file_NO =0;
open(OUT,">Test.txt");
while ($count1 <= $file_NO ){
#print"\n\n"; print my $file = "$count1.txt";
open(load,$file);
my $input; my $MULcount11; my @load11; my $incount = 0;
while ($input = <load>){
chomp ($input);
print $load11[$MULcount11] = $input,"\n";
     if (length($load11[$MULcount11]) <= 1) {
          seq(); #print OUT "\n"; }
$MULcount11++; }
seq();
sub seq
{
$MULcount11 = -1 ; my $Seq  ; shift(@load11);
$Seq = join(",@load11); $Seq =~ s/-//g;
$Seq =~ s/[a-z]//g;
print OUT $Seq;
if( $incount == 1) {
print OUT "\n";}
$incount++;}
print OUT "\n\n";
close (load);
$count1++;
}
# generating a set of random numbers
srand(time|$$);
my @numbers; my @sorted =0 ;
for(my $i = 0; $i < 10; $i++){
          my $num = int(rand(100));
my $numb = $num."\n"; $numbers[$i] = $numb;}
print @numbers, "\n"; @sorted = insort(@numbers);
print @sorted, "\n";
##########################################################################
#SUBROUTINES
##########################################################################
sub insort{
my @sorted = @_; my $len = (@sorted-1); my $i; my $j;
 for ($i = 0; $i < $len; $i++){
                    $j = $i;
                    while (($j >= 0) && ($sorted[$j+1] < $sorted[$j])){
                              my $tmp = $sorted[$j+1];
```

```
                        $sorted[$j+1] = $sorted[$j];
                            $sorted[$j] = $tmp;
                            $j--;}}return @sorted; }

open (LOAD,"Test.txt");
open (OUT,">output.txt");
while ($Alphabet = <LOAD>){
if ($Alphabet ne "\n"){
$DNA = join(",$Alphabet);  $DNA =~ s/\s//g;
@Alphabet = split(",$DNA),"\n"; $L= (@Alphabet+1-1);
$S = randstring($L);
print OUT $S,"\n";
sub randstring {
$Z = @_; $i = 0; $C = ''; $A = @Alphabet;
while ( $i < $L ){ $i = $i + 1;
$Die = int rand($A); $C = $C . $Alphabet[$Die],"\n";}
return $C; }}   }
exit;
 #!/usr/bin/perl
#use warnings;
#use diagnostics;
use strict;
use DBI;
# GLOBAL VARIABLES
#=================
#my $union = 'FALSE'; #my $intersection = 'TRUE';
my $wild_seq = 'TRUE'; my $funcMUT_seq = 'TRUE';  my $NONfuncMUT_seq = 'TRUE'; my @spp; my $WS;
my @WS; my $ALL_FUN; my @ALL_FUN;
my $MULcount11 = 0; my @load11; my $no_more_load; my $length_AVI;
 my $STAT2 = 4.7;
#connect to database
my $dbh = DBI->connect('DBI:mysql:mrpap:kas.wku.edu','root','') or die "Can't connect to database!\n";
#grab scaletable information from database
my $sql = "Node,Ala,Arg,Asn,Asp,Cys,Gln,Glu,Gly,His,Ile,Leu,Lys,Met,Phe,Pro,Ser,
Thr, Trp,Tyr,Val FROM SCALETABLE order by Node";
my $sth = $dbh->prepare($sql) or die "Can't prepare $sql" . $dbh->errstr. "\n";
$sth->execute or die "Can't execute $sql:".$dbh->errstr."\n"; my $numcols = $sth->rows;
my(@node,@ala,@arg,@asn,@asp,@cys,@gln,@glu,@gly,@his,@ile,@leu,@lys,@met,@phe,@pro,@ser,@thr,
@trp,@tyr,@val);
    while( my @row = $sth->fetchrow_array) {
            push @node,$row[0];push @ala,$row[1] ;push @arg,$row[2] ;push @asn,$row[3] ;push @asp,$row[4];
            push @cys,$row[5] ;push @gln,$row[6] ;push @glu,$row[7] ;push @gly,$row[8] ;push @his,$row[9];
            push @ile,$row[10];push @leu,$row[11];push @lys,$row[12];push @met,$row[13];push
@phe,$row[14];
            push @pro,$row[15];push @ser,$row[16];push @thr,$row[17];push @trp,$row[18];push @tyr,$row[19];
            push @val,$row[20];
        }#end while
$dbh-> disconnect; # at present# OPEN THE FILE FOR LOADING THE SEQUENCE INFORMAION
open (LOAD,"Test.txt");
     while (my $test11 = <LOAD>){
            chomp ($test11);
           $load11[$MULcount11] = $test11; $length_AVI = $load11[0];
if (length($load11[$MULcount11]) <= 1) {
test ();
$no_more_load = 0; }
$MULcount11++;}
```

```
#=========================================
# TEST Function DOES THE ACTUAL COMPUTATION
#=========================================
sub test{
my $while_loop_count = $MULcount11; my $load2d = $MULcount11;
my $Wloop_count1 = 0; my @WFun_spp = 0; my $spp_count = 0;
my $WFun_count = 0; $MULcount11 = -1;
# MAIN LOOP
while ($Wloop_count1 < $while_loop_count-1) {
my $Wloop_count2 = $Wloop_count1;
#Process SEQUENCE Infromation'
if ($wild_seq eq 'TRUE') {
$WS = ("$load11[$Wloop_count1]"); @WS = split(/\r\n/,$WS); #shift @WS;
 $WS = join('',@WS); @WS = split(//,$WS),"+++++\n";}
# SECOND LOOP
while ($Wloop_count2+1 < $while_loop_count) {if ($funcMUT_seq eq 'TRUE')
{$ALL_FUN = ("$load11[$Wloop_count2+1]"); @ALL_FUN = split (/\r\n/,$ALL_FUN); #shift @ALL_FUN;
$ALL_FUN = join('', @ALL_FUN); @ALL_FUN = split(//,$ALL_FUN),"\n";}
#############################################################################
#convert AA sequences to 2d arrays with scaletable information
my @ convertseq(\@WS,\@node,\@ala,\@arg,\@asn,\@asp,\@cys,\@gln,\@glu,\@gly,
\@his,\@ile,\@leu,\@lys,\@met,\@phe,\@pro,\@ser,\@thr,\@trp,\@tyr,\@val,1);
my @ALL_ convertseq(\@ALL_FUN,\@node,\@ala,\@arg,\@asn,\@asp,\@cys,\@gln,
\@glu,\@gly,\@his,\@ile,\@leu,\@lys,\@met,\@phe,\@pro,\@ser,\@thr,\@trp,\@tyr,\@val,1);
#=============================================================
# convertseq
# This subroutine converts an array of characters into a 2d array
# indexed by [position][node]
# As input, you must first provide a reference to the array that contains the
# character sequence information. Then you must also provide a reference to
# each of the arrays: @node,@ala,@arg,.....,@val The final argument is a boolean
# (1 or 0) that determines if an HTML table with the results is printed to STDOUT
#=============================================================
sub convertseq {
my($WSr,$noder,$alar,$argr,$asnr,$aspr,$cysr,$glnr,$glur,$glyr,$hisr,$iler,$leur,$lysr,$metr,$pher,
$pror,$serr,$thrr,$trpr,$tyrr,$valr,$printtable) = @_;
#convert references to useable arrays
my @WS = @$WSr;my @node = @$noder;my @ala = @$alar;my @arg = @$argr;my @asn = @$asnr; my @asp
= @$aspr;my @cys = @$cysr;my @gln = @$glnr;my @glu = @$glur;my @gly = @$glyr; my @his = @$hisr;my
@ile = @$iler;my @leu @$leur;my @lys = @$lysr;my @met = @$metr; my @phe = @$pher;my @pro =
@$pror;my @ser = @$serr;my @thr = @$thrr;my @trp = @$trpr; my @tyr = @$tyrr;my @val = @$valr;
#convert character sequence to 2D array
my @WS2;
for(my $pos=0;$pos<@WS;$pos++) {if($WS[$pos] eq "A") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] =
$ala[$n]; }}
if($WS[$pos] eq "R") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $arg[$n]; }}
if($WS[$pos] eq "N") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $asn[$n]; }}
if($WS[$pos] eq "D") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $asp[$n]; }}
if($WS[$pos] eq "C") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $cys[$n]; }}
if($WS[$pos] eq "Q") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $gln[$n]; }}
if($WS[$pos] eq "E") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $glu[$n]; }}
if($WS[$pos] eq "G") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $gly[$n]; }}
if($WS[$pos] eq "H") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $his[$n]; }}
if($WS[$pos] eq "I") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $ile[$n]; }}
if($WS[$pos] eq "L") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $leu[$n]; }}
if($WS[$pos] eq "K") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $lys[$n]; }}
```

```
if($WS[$pos] eq "M") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $met[$n]; }}
if($WS[$pos] eq "F") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $phe[$n]; }}
if($WS[$pos] eq "P") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $pro[$n]; }}
if($WS[$pos] eq "S") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $ser[$n]; }}
if($WS[$pos] eq "T") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $thr[$n]; }}
if($WS[$pos] eq "W") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $trp[$n]; }}
if($WS[$pos] eq "Y") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $tyr[$n]; }}
if($WS[$pos] eq "V") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $val[$n]; }}
}#end for
if($printtable) {for(my $aa=0;$aa<@WS;$aa++) {}for(my $j=0;$j<@node;$j++){
for(my $i=0;$i<@WS;$i++) {}}}#end if @WS2; #return 2d array}
# variable to load the.  my @fpp1;
# COMPUTATION FOR SPP BETWEEN WILD AND FUNCTIONAL SEQUENCES
if ($wild_seq eq 'TRUE'&& $funcMUT_seq eq 'TRUE') { my $STAT11 = 4.07;
my $numcols = 448; my @fun_ppool; # I dont know for what this variable is. my $k=0;
my $count = 1; my @array1; my $avi; my @fpp2;
for(my $pos = 0; $pos<@WS2; $pos++){@array1 = 0; $array1[0] = $pos + 1;
for(my $nodeN = 0; $nodeN<$numcols;$nodeN++){
my $avi = abs($WS2[$pos][$nodeN] - $ALL_FUN2[$pos][$nodeN]);
if($avi <= $STAT11) {
$avi =  ("$node[$nodeN]"); $array1[$count] = ("$avi");$count++;}}#end for
$spp[$WFun_count][$pos]  =  [@array1];
# THE BELOW PRINT FUNCTION PRINTS THE FPP POOL
$count = 1; }#end for
print $WFun_count++,"avi\n";}
#print " @WS **@ALL_FUN\n";$Wloop_count2++;}#END OF THE SECOND LOOP
$Wloop_count1++;}# END OF THE MAIN LOOP
intersection();
#INTERSECTION
#============
sub intersection{
my $length1 = length($length_AVI); my @intersection; my @spp1; my @spp2;
 my @LOADintersection; my @final_intersection; #my $countLOAD = 0;
 for (my $countLOAD = 0; $countLOAD <= $length1-1; $countLOAD++){
$countLOAD; my $countLOAD1 = 0;
while ($countLOAD1 <= $load2d-1) {my $ref1; my $ref2; if ($countLOAD1 <=0) {
$ref1 = $spp[0][$countLOAD]; @spp1 = @$ref1,"\n";shift (@spp1); $ref2 = $spp[1][$countLOAD]; @spp2 =
@$ref2,"\n";shift (@spp2); }
   if ($countLOAD1 > 0) {
   $ref1 = $LOADintersection[$countLOAD]; @spp1 = @$ref1,"\n";shift (@spp1);
   $ref2 = $spp[$countLOAD1][$countLOAD]; @spp2 = @$ref2,"\n";shift (@spp2); }
   my $count = 1; @intersection = 0; $intersection[0] = $countLOAD + 1;
   @LOADintersection =0;
   for (my $count1 = 0; $count1 <= 447; $count1++){
   for (my $count2 = 0; $count2 <= 447;$count2++){if($spp2[$count2] ==
   $spp1[$count1]) {$intersection[$count] = $spp1[$count1]; $count++;}}}
$countLOAD1++; $LOADintersection[$countLOAD ] = [@intersection]; }
$final_intersection[$countLOAD] = $LOADintersection[$countLOAD]; }
subsitution (@final_intersection); }
#SUBINDEX
sub subsitution{
my (@input_fpp)=@_ ;
my $dbh= DBI->connect ("DBI:mysql:mrpap:kas.wku.edu",'root','');
#grab aatranslation info and put into a hash
my $sql = "select One_Letter,Three_Letter from aatranslation";
my $sth= $dbh->prepare ($sql) or die "Can't prepare $sql: "  . $dbh->errstr  . "\n";
```

```
$sth->execute or die "Can't execute $sql: " . $dbh->errstr . "\n";
my @row; my(%aatranslate,%aatranslate2);
while(@row=$sth->fetchrow_array) {
$aatranslate{$row[0]} = $row[1]; $aatranslate2{$row[1]} = $row[0]; }
#create & initialize 2d array for saving sums
# WHAT IS HAPPENING HERE IS ZEROS ARE BEING FILLED TO INITILIZE THE 2D # ARRAY WITH
ZERO BEFORE FILLING IT WITH THE PERCENTAGES.
my @si;
for(my $p=0;$p<length($length_AVI);$p++) { for(my $aa=0;$aa<20;$aa++) { $si[$p][$aa] = 0; }}
#Removing position from FPP table
# THE MAIN LOOP RUNS FOR SIX TIMES FOR THE GIVEN LENGTH OF
SEQUENCE
#my @Seq_Name; my @Seq_Name = split (//,"$length_AVI");my ($ref,@a,$pos);
 print"\n";print"\n"; print "A || C || D || E || F || G || H || I || K || L || M || N || P || Q || R || S || T ||
V || W || % Value fo SI \n";
for (my $j=0;$j<length($length_AVI);$j++){$ref = $input_fpp[$j]; @a= @$ref;
print"\n";print@$ref,"\n"; $pos = shift @a;
# IT REMOVES THE POSITION NUMBER FROM THE FPP ARRAY
my $wildaa = $aatranslate{substr($length_AVI,$pos-1,1)}; # TAKES THE THREE LETTER ABB OF THE
SEQUENCE FORM S.TABLE
$sql = $wildaa,Ala,Cys,Asp,Glu,Phe,Gly,His,Ile,Lys,Leu,Met,Asn,Pro,Gln,Arg,Ser,Thr,
Val, Trp,Tyr from scaletable where node = '";$sql .= join("' or node='",@a); $sql .= "'";
$sth= $dbh->prepare ($sql) or die "Can't prepare $sql: "  . $dbh->errstr  . "\n";
$sth->execute or die "Can't execute $sql: " . $dbh->errstr . "\n"; my $cnt=0;
while(@row=$sth->fetchrow_array) {
$cnt++; $wildaa = shift @row;
#print@row,"\n"; #print $wildaa,"\n\n";
for(my $i=0;$i<@row;$i++){ if((abs($row[$i] - $wildaa)) <= 7.6) { $si[$pos-1][$i] += 1; }}}print"\n";my $si;
print $Seq_Name[$pos-1],"      ";# FOR PRINTIN THE SEQ LETTERS ON OUTPUT
for(my $aa=0;$aa<20;$aa++){ $ref = $input_fpp[$pos-1]; @a = @$ref;
$si[$pos-1][$aa] = ($si[$pos-1][$aa]/(@a-1)*100);
print int($si[$pos-1][$aa]);print "  "; $si = $si + $si[$pos-1][$aa]; } my $SI = ($si/20);
print "    %SI for position ",$pos," is ",$SI," "; # Gives the %SI}} # End of the function substitution.
$dbh-> disconnect;
}# END OF THE TEST FUNCTION
exit;
```

```
#=================================================================
# Program Description: The program implements the function which computes the
#                      amino acid profiles and sends the output to the file.
#=================================================================
#!/usr/bin/perl
use strict; use DBI;
# GLOBAL VARIABLES
#=================
#my $union = 'FALSE'; #my $intersection = 'TRUE'; my $wild_seq = 'TRUE';
 my $funcMUT_seq = 'TRUE'; my $NONfuncMUT_seq = 'TRUE';
my @spp; my $WS; my @WS; my $ALL_FUN; my @ALL_FUN;
my $MULcount11 = 0; my @load11; my $no_more_load; my $length_AVI;
my $STAT2 = 1; my $set_count = 0;
open (OUT,">results.txt");
#connect to database
my $dbh = DBI->connect('DBI:mysql:mrpap:kas.wku.edu','root','') or die "Can't connect to database!\n";
my $sql = "SELECT Node,Ala,Arg,Asn,Asp,Cys,Gln,Glu,Gly,His,Ile,Leu,Lys,Met,Phe,
Pro,Ser,Thr, Trp,Tyr,Val FROM NEWSCALETABLE order by Node";
my $sth = $dbh->prepare($sql) or die "Can't prepare $sql" . $dbh->errstr. "\n";
$sth->execute or die "Can't execute $sql:".$dbh->errstr."\n"; my $numcols = $sth->rows;
my (@node,@ala,@arg,@asn,@asp,@cys,@gln,@glu,@gly,@his,@ile,@leu,@lys,
@met,@phe,@pro,@ser,@thr,@trp,@tyr,@val);
 while( my @row = $sth->fetchrow_array) {chomp(@row);
push @node,$row[0];push @ala,$row[1] ;push @arg,$row[2] ;push @asn,$row[3] ;push @asp,$row[4]; push
@cys,$row[5] ;push @gln,$row[6] ;push @glu,$row[7] ;
@gly,$row[8] ;push @his,$row[9]; push @ile,$row[10];push @leu,$row[11];push @lys,$row[12];push
@met,$row[13];push @phe,$row[14]; push @pro,$row[15];push @ser,$row[16];push @thr,$row[17];push
@trp,$row[18];push @tyr,$row[19];
 push @val,$row[20]; }#end while
$dbh-> disconnect; # at present# OPEN THE FILE FOR LOADING THE SEQUENCE INFORMAION
       open (LOAD,"Test.txt");
       while (my $test11 = <LOAD>){chomp ($test11);
              $load11[$MULcount11] = $test11; $length_AVI = $load11[0];
                if (length($load11[$MULcount11]) <= 1) {
                test ();
              $no_more_load = 0; }
$MULcount11++;}
# TEST Function DOES THE ACTUAL COMPUTATION
sub test{my $while_loop_count = $MULcount11; my $load2d = $MULcount11;
my $Wloop_count1 = 0; my @WFun_spp = 0; my $spp_count = 0;
my $WFun_count = 0; $MULcount11 = -1;
# MAIN LOOP
while ($Wloop_count1 < $while_loop_count-1) { my $Wloop_count2 = $Wloop_count1;
#Process SEQUENCE Infromation'
if ($wild_seq eq 'TRUE') {$WS = ("$load11[$Wloop_count1]");                    @WS = split(/\r\n/,$WS);
#shift @WS;
$WS = join(",@WS); @WS = split(//,$WS),"+++++\n";}# SECOND LOOP
while ($Wloop_count2+1 < $while_loop_count) {if ($funcMUT_seq eq 'TRUE') {
$ALL_FUN = ("$load11[$Wloop_count2+1]"); @ALL_FUN = split (/\r\n/,$ALL_FUN);
#shift @ALL_FUN; $ALL_FUN = join(", @ALL_FUN); @ALL_FUN = split(//,$ALL_FUN),"\n";}#convert AA
sequences to 2d arrays with information
my @ convertseq(\@WS,\@node,\@ala,\@arg,\@asn,\@asp,\@cys,\@gln,\@glu,\@gly,
\@his,\@ile,\@leu,\@lys,\@met,\@phe,\@pro,\@ser,\@thr,\@trp,\@tyr,\@val,1);
my @ALL_ convertseq(\@ALL_FUN,\@node,\@ala,\@arg,\@asn,\@asp,\@cys,\@gln,\
@glu,\@gly,\@his,\@ile,\@leu,\@lys,\@met,\@phe,\@pro,\@ser,\@thr,\@trp,\@tyr,\@val,1);
sub convertseq {
```

```
my($WSr,$noder,$alar,$argr,$asnr,$aspr,$cysr,$glnr,$glur,$glyr,$hisr,$iler,$leur,$lysr,$metr,$pher,
$pror,$serr,$thrr,$trpr,$tyrr,$valr,$printtable) = @_;
#convert references to useable arrays
my @WS = @$WSr;my @node = @$noder;my @ala = @$alar;my @arg = @$argr;my @asn = @$asnr; my @asp
= @$aspr;my @cys = @$cysr;my @gln = @$gln@$glur;my @gly = @$glyr;my @his = @$hisr;my @ile =
@$iler;my @leu = @$leur;my
@lys = @$lysr; my @met = @$metr; my @phe = @$pher;my @pro = @$pror;my @ser = @$serr;my @thr =
@$thrr;my @trp = @$trpr; my @tyr = @$tyrr;my @val = @$valr;
#convert character sequence to 2D array
my @WS2;
 for(my $pos=0;$pos<@WS;$pos++) {if($WS[$pos] eq "A") {
for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $ala[$n]; }}
if($WS[$pos] eq "R") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $arg[$n]; }}
if($WS[$pos] eq "N") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $asn[$n]; }}
if($WS[$pos] eq "D") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $asp[$n]; }}
if($WS[$pos] eq "C") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $cys[$n]; }}
if($WS[$pos] eq "Q") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $gln[$n]; }}
if($WS[$pos] eq "E") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $glu[$n]; }}
if($WS[$pos] eq "G") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $gly[$n]; }}
if($WS[$pos] eq "H") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $his[$n]; }}
if($WS[$pos] eq "I") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $ile[$n]; }}
if($WS[$pos] eq "L") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $leu[$n]; }}
if($WS[$pos] eq "K") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $lys[$n]; }}
if($WS[$pos] eq "M") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $met[$n]; }}
if($WS[$pos] eq "F") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $phe[$n]; }}
if($WS[$pos] eq "P") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $pro[$n]; }}
if($WS[$pos] eq "S") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $ser[$n]; }}
if($WS[$pos] eq "T") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $thr[$n]; }}
if($WS[$pos] eq "W") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $trp[$n]; }}
if($WS[$pos] eq "Y") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $tyr[$n]; }}
if($WS[$pos] eq "V") {for(my $n=0;$n<@node;$n++) {$WS2[$pos][$n] = $val[$n]; }}
}#end for
if($printtable) {for(my $aa=0;$aa<@WS;$aa++) {}
for(my $j=0;$j<@node;$j++){for(my $i=0;$i<@WS;$i++) {}}
}#end if
@WS2; #return 2d array}
# variable to load the.
my @fpp1;
# COMPUTATION FOR SPP BETWEEN WILD AND FUNCTIONAL MUTANT SEQUENCES
if ($wild_seq eq 'TRUE'&& $funcMUT_seq eq 'TRUE') {
my $STAT11 = 1; my $numcols = 494; my @fun_ppool; my $k=0; my $count = 1;
my @array1; my $avi; my @fpp2;
#my $WFun_count = 0;
for(my $pos = 0; $pos<@WS2; $pos++){
@array1 = 0; $array1[0] = $pos + 1;
for(my $nodeN = 0; $nodeN<$numcols;$nodeN++){
my $avi = abs($WS2[$pos][$nodeN] - $ALL_FUN2[$pos][$nodeN]);
if($avi <= $STAT11) {$avi =  ("$node[$nodeN]"); $array1[$count] = ("$avi");
chomp ($array1[$count]); $count++;}}#end for shift (@array1);
 #$WFun_spp[$pos]=  [@array1]; $spp[$WFun_count][$pos]  =  [@array1];
#my $ref1 = $spp[$WFun_count][$pos];
#print my @fpp1 = @$ref1,"\n"; print
# THE BELOW PRINT FUNCTION PRINTS THE FPP POOL
#print @array1,"\n";
 $count = 1; }#end for
$WFun_count++;
```

```
#subsitution (@spp); }
#print " @WS **@ALL_FUN\n"; $Wloop_count2++;}#END OF THE SECOND LOOP
$Wloop_count1++;}# END OF THE MAIN LOOP
intersection();
#INTERSECTION
#============
sub intersection{
my $length1 = length($length_AVI); my @intersection; my @spp1; my @spp2;
 my @LOADintersection; my @final_intersection;
#my $countLOAD = 0;
 for (my $countLOAD = 0; $countLOAD <= $length1-1; $countLOAD++){
#$countLOAD;
my $countLOAD1 = 0;
while ($countLOAD1 <= $load2d-1) {
my $ref1; my $ref2;
if ($countLOAD1 <=0) {$ref1 = $spp[0][$countLOAD]; @spp1 = @$ref1;
shift (@spp1); $ref2 = $spp[1][$countLOAD]; @spp2 = @$ref2; shift (@spp2); }
if ($countLOAD1 > 0) {$ref1 = $LOADintersection[$countLOAD]; @spp1 = @$ref1;
 shift (@spp1); $ref2 = $spp[$countLOAD1][$countLOAD]; @spp2 = @$ref2; shift (@spp2); }
my $count = 1; @intersection = 0; $intersection[0] = $countLOAD + 1; @LOADintersection =0;
for (my $count1 = 0; $count1 <= (@spp1-2); $count1++){
for (my $count2 = 0; $count2 <= (@spp2-2);$count2++){
if($spp2[$count2] == $spp1[$count1]) { $intersection[$count] = $spp1[$count1]; $count++;$count2 = (@spp2-1);
}}}
$countLOAD1++;$LOADintersection[$countLOAD ] = [@intersection]; }
my $ref1 =  $final_intersection[$countLOAD] = $LOADintersection[$countLOAD];
 my @fpp1 = @$ref1;
                }
#chomp (@final_intersection);  subsitution (@final_intersection); }
#==============
#SUBINDEX
#==============
sub subsitution{
my (@input_fpp)=@_ ; $set_count++;
my $dbh= DBI->connect ("DBI:mysql:mrpap:kas.wku.edu",'root','');
#grab aatranslation info and put into a hash
my $sql = "select One_Letter,Three_Letter from aatranslation";
my $sth= $dbh->prepare ($sql) or die "Can't prepare $sql: "  . $dbh->errstr  . "\n";
$sth->execute or die "Can't execute $sql: " . $dbh->errstr . "\n";
my @row; my(%aatranslate,%aatranslate2);
while(@row=$sth->fetchrow_array) {
$aatranslate{$row[0]} = $row[1]; $aatranslate2{$row[1]} = $row[0]; }
#create & initialize 2d array for saving sums
# ARRAY WITH ZERO BEFORE FILLING IT WITH THE PERCENTAGES.
my @si;  for(my $p=0;$p<length($length_AVI);$p++) {
for(my $aa=0;$aa<20;$aa++) { $si[$p][$aa] = 0; }}
#Removing position from FPP table
# THE MAIN LOOP RUNS FOR SIX TIMES FOR THE GIVEN LENGTH OF THE SEQUENCE
#my @Seq_Name; my @Seq_Name = split (//,"$length_AVI");
 my ($ref,@a,$pos); #print OUT"\n\n";
 #print OUT " THE NUMBER OF THE SET IS  $set_count \n\n"; #print OUT  #print OUT "A| |C| |D| |E| |F| |G| |H|
|I| |K| |L| |M| |N| |P| |Q| |R| |S| |T| |V| |W| |Y                % Value fo SI \n";
 #print OUT #print OUT "\n  ";
for (my $j=0;$j<length($length_AVI);$j++){$ref = $input_fpp[$j]; @a= @$ref;
#print my $isthere =(@a-1),"     \n"; #print OUT "\n"; @$ref; chomp (@a);
 print OUT "\n"; $pos = shift @a; # IT REMOVES THE POSITION NUMBER FROM
```

```
my $wildaa = $aatranslate{substr($length_AVI,$pos-1,1)}; # TAKES THE THREE LETTER ABB OF THE
SEQUENCE FORM S.TABLE
$sql = " $wildaa,Ala,Cys,Asp,Glu,Phe,Gly,His,Ile,Lys,Leu,Met,Asn,Pro,Gln,Arg,Ser,
Thr,Val,Trp,Tyr from NEWSCALETABLE where node = '";
$sql .= join("' or node='",@a); $sql .= "';$sth= $dbh->prepare ($sql) or die "Can't prepare $sql: "  . $dbh->errstr  .
"\n";$sth->execute or die "Can't execute $sql: " . $dbh->errstr . "\n"; my $cnt=0;
# THIS LOOP ALLOWS EQUAL TO NODE TURNS. 001,002 TOTAL TURNS = TO NO OF NODES IN THAT
POSITION IF FPP (PER ONE Fpp)
 while(@row=$sth->fetchrow_array) {chomp (@row);
 $cnt++;
 $wildaa = shift @row; @row; $wildaa;
# THIS LOOP RUNS FOR 20 TIMES
for(my $i=0;$i<@row;$i++) my $avi = $row[$i] - $wildaa; $avi = abs ($avi);
if( $avi <= 1) {
#print $avi,"asdfasdfas  $pos-1  fsdfasfasfsa $i  dfsadfsdfasadffsad\n"; $si[$pos-1][$i] += 1; }}}
my $si; # print OUT $Seq_Name[$pos-1],"      ";# FOR PRINTIN THE SEQ LETTERS ON THE OUTPUT
my $seecount =0; for(my $aa=0;$aa<20;$aa++){ $ref = $input_fpp[$pos-1];
@a = @$ref; my $check = (@a-1); #$si[$pos-1][$aa],"      $check    \n"; $si[$pos-1][$aa] = ($si[$pos-1][$aa]/(@a-
1)*100); my $cutoff = $si[$pos-1][$aa]; int ($cutoff);  if($cutoff >= 92 && $cutoff <= 99) {if ($pos != ($aa+1)
)#&& $seecount <= 1 ) {
print OUT int ($cutoff)," ";print OUT $pos ," ", $aa+1,"  " ; if ($aa+1 == 1){print OUT "A ";};if ($aa+1 == 2){print
OUT "C ";};if ($aa+1 == 3){print OUT "D ";};
if ($aa+1 == 4){print OUT "E ";};if ($aa+1 == 5){print OUT "F ";};
if ($aa+1 == 6){print OUT "G ";};if ($aa+1 == 7){print OUT "H ";};if ($aa+1 == 8){print OUT "I ";};if ($aa+1 ==
9){print OUT "K ";};if ($aa+1 == 10){print OUT "L ";};if ($aa+1 == 11){print OUT "M ";};if ($aa+1 == 12){print
OUT "N ";};if ($aa+1 == 13){print OUT "P ";};if ($aa+1 == 14){print OUT "Q ";};if ($aa+1 == 15){print OUT "R
";};if ($aa+1 == 16){print OUT "S ";};if ($aa+1 == 17){print OUT "T ";};if ($aa+1 == 18){print OUT "V ";};if
($aa+1 == 19){print OUT "W ";};if ($aa+1 == 20){print OUT "Y ";}; #$seecount++;} print OUT "\n";}}}
$dbh-> disconnect;
 } # End of the function substitution. }# END OF THE TEST FUNCTION
exit;
#=================================================================
# Program Description: The Program implements the calculation of the percentage
#                              of nuclic acids in the given sequence.
#=================================================================
#!usr/local/bin/perl –w
use strict;
my $DNA = "DNA.txt";
chomp($DNA);
print "The percentage of 'A' is ",&PercentageA($DNA),"%\n\n";
sub PercentageA(){my $input = @_; unless (open(LOAD,$DNA)) {
print "Cannot open file \"$DNA\"\n\n";return 0; }
my @DNA; @DNA = <LOAD>; close LOAD;
my $DNA = join('',@DNA); $DNA =~ s/\s//g; @DNA = split('',$DNA);
if((@DNA) < 1) {print "The file has a Zero size\n\n";exit; }
my $count_of_A = 0; foreach my $base(@DNA) {if($base eq 'A') {
$count_of_A++;}}my $percent = $count_of_A / (@DNA-1+1)*100; return $percent; }
```

```
#=============================================================
# Program Description: The program tests the Data Base connectivity.
#=============================================================
#usr/local/bin/perl
use DBI;
my $dbh = DBI->connect('DBI:mysql:mrpap:kas.wku.edu','root','') or die "Can't connect to database!\n";
#grab scaletable information from database
my $sql = "SELECT Node,Ala,Arg,Asn,Asp,Cys,Gln,Glu,Gly,His,Ile,Leu,Lys,Met,Phe,
Pro,Ser,Thr,Trp,Tyr,Val FROM SCALETABLE order by Node";
my $sth = $dbh->prepare($sql) or die "Can't prepare $sql" . $dbh->errstr. "\n";
$sth->execute or die "Can't execute $sql:".$dbh->errstr."\n";
my $numcols = $sth->rows;
print "$numcols"; $sth->finish;
$dbh->disconnect;
# Avinash M. Baktula
# Implementing Program which creates a local data and generates Random DNA
   sequences
# usr/bin/perl –w
use strict;
# Generate 10 random DNA sequences named dna0 through dna9 with lengths between
# 12 and 18 nucleotides which are multiples of 3 and write the dna sequences
# into a dbm database file # Declare and initialize variables
my $size_set = 10; my $max_length = 18; my $min_length = 12; my $name;
my %random_dna = ();
# Get seed for random number generator using system time srand(time|$$);
%random_dna = make_rand_dnaset($min_length, $max_length, $size_set);
#print %random_dna;
# store the results, one per line, in a dbm database file
dbmopen(%random_dna,'rand_dna_set', 0644) or die ("cannot create rand_dna_set $!");
dbmclose(%random_dna);
dbmopen(%random_dna,'rand_dna_set', 0644);
print %random_dna;
dbmclose(%random_dna);
exit;
# subroutine to create a random DNA set
# sub make_rand_dnaset
sub make_rand_dnaset {
my($min_length, $max_length, $size_set) = @_;
my $length; my %set; my $dna;
# Create set
for(my $i = 0; $i < $size_set; ++$i){
#pick a random number between 0 and 2 my $mult = int(rand(3));
# make random dna fragment
$length = $min_length + 3* $mult; $dna = make_rand_dna($length);
my $avi = "AVI$i";
#give dna a name
$name = $avi;
#store dna and name in hash
$set{$name} = "$dna\n";}return %set; }
# Subroutine to make a random DNA fragment
# Sub make_rand_dna
sub make_rand_dna { my($length) = @_;my $dna;
 for (my $i = 0; $i < $length; $i++){$dna .= rand_nuc();}
return $dna; }# Subroutine to select a random nucleotide sub rand_nuc
sub rand_nuc{my (@nuc) = ('A', 'C', 'G', 'T');
my $i = int(rand(4)); return $nuc[$i]; }
```

```
#=================================================================
# Program Description: The program implements the function which generates Protein
                       sequence for an DNA sequence.
#=================================================================
#! usr/bin/perl -w
use strict;
use warnings;
# transcribe DNA into corresponding aminoacids read DNA sequence from file
print "Please enter filename to open:"; my $dna_file = <STDIN>; chomp $dna_file;
unless (-e $dna_file){ print "File $dna_file does not seem to exist!!\n"; exit; }
unless (open(DNAFILE, $dna_file)){ print "Cannot open $dna_file!!\n"; exit; }
my $dna = <DNAFILE>;close DNAFILE; $dna =~  s/^\s$//;chomp $dna;
my $len = length($dna); my $pep = ''; my @peptide = (); my $count = 0;
# Translate each 3 nucleotide codon to an aminoacid to make a peptide chain
for(my $i = 0; $i < $len-2 ; $i +=3){ my $codon = substr($dna, $i, 3); my $pep = codon2aa($codon); my $codonpep
= "$codon($pep) "; $peptide[$count] = ($codonpep);
$count++;}print "\n"; print "The codons from the DNA sequence and corresponding amino acids (in parentheses)
are: \n"; print "\n"; my $amino = join('', @peptide);
my $j; my $length = length($amino);
# Printing each 3 nucleotide codon followed by its corresponding amino acid (in # parentheses) to a total of 4
codons per line
for ($j = 0; $j < $length; $j += 28){ print substr($amino, $j, 28), "\n";}print "\n"; exit;
#SUBROUTINE
# subroutine to convert the 3 nucleotide codon in dna to an amino acid
sub codon2aa{ my($codon) = @_;
if ($codon =~ /GC./i)   {return 'A'}    # Alanine
elsif ($codon =~ /TG[TC]/i)    {return 'C'}    # Cysteine
elsif ($codon =~ /GA[TC]/i)    {return 'D'}    # Aspartic acid
elsif ($codon =~ /GA[AG]/i)    {return 'E'}    # Glutamic acid
elsif ($codon =~ /TT[TC]/i)    {return 'F'}    # Phenylalanine
elsif ($codon =~ /GG./i)       {return 'G'}    # Glycine
elsif ($codon =~ /CA[TC]/i)    {return 'H'}    # Histidine
elsif ($codon =~ /AT[TCA]/i)   {return 'I'}    # Isoleucine
elsif ($codon =~ /AA[AG]/i)    {return 'K'}    # Lysine
elsif ($codon =~ /TT[AG]|CT./i)        {return 'L'}    # Leucine
elsif ($codon =~ /ATG/i)       {return 'M'}    # Methionine
elsif ($codon =~ /AA[TC]/i)    {return 'N'}    # Asparagine
elsif ($codon =~ /CC./i)       {return 'P'}    # Proline
elsif ($codon =~ /CA[AG]/i)    {return 'Q'}    # Glutamine
elsif ($codon =~ /CG.|AG[AG]/i)        {return 'R'}    # Arginine
elsif ($codon =~ /TC.|AG[TC]/i)        {return 'S'}    # Serine
elsif ($codon =~ /AC./i)       {return 'T'}    # Throenine
elsif ($codon =~ /GT./i)       {return 'V'}    # Valine
elsif ($codon =~ /TGG/i)       {return 'W'}    # Tryptophan
elsif ($codon =~ /TA[TC]/i)            {return 'Y'}          # Tyrosine
elsif ($codon =~ /TA[AG]|TGA/i)   {return '_'}          #stop else {
print STDERR "Bad Codon \"$codon\" !! \n";exit; }}

#=================================================================
# Program Description: The program implements the function which sorts the GI NO
#=================================================================
#! usr/bin/perl -w
use strict;
# generating a set of random numbers
srand(time|$$); my @numbers; my @sorted;
for(my $i = 0; $i < 10; $i++){my $num = int(rand(100)); my $numb = $num."\n";
```

```
$numbers[$i] = $numb;} print "Input list of numbers: \n"; print @numbers;
print "Sorted list of numbers: \n"; @numbers = selsort(@numbers);
print @numbers;
#SUBROUTINES
# Subroutine for selection sort algorithm
sub selsort{
my(@numbers) = @_;my $len = @numbers; my $i; my $j = 1;my $pos;
for ($i = 0; $i <= $len-1; $i++){my $ref = $numbers[$i];
for ($j = $i+1; $j < $len; $j++){if ($numbers[$j] < $ref){ $ref = $numbers[$j];
$pos = $j; }}my $temp = $numbers[$i]; $numbers[$i] = $ref; if($temp != $numbers[$i]){$numbers[$pos] = $temp;}
}return @numbers; }
```

```
#=================================================================
# Program Description: The program implements the generation of the Graphs
#=================================================================
use GD;
# create a new image
$im = new GD::Image(100,100);
# allocate some colors
$white = $im->colorAllocate(255,255,255); $black = $im->colorAllocate(0,0,0);          $red = $im-
>colorAllocate(255,0,0); $blue = $im->colorAllocate(0,0,255);
# make the background transparent and interlaced
$im->transparent($white); $im->interlaced('true');
# Put a black frame around the picture
$im->rectangle(0,0,99,99,$black);
# Draw a blue oval
$im->arc(50,50,95,75,0,360,$blue);
# And fill it with red
$im->fill(50,50,$red);  # make sure we are writing to a binary stream binmode STDOUT;
# Convert the image to PNG and print it on standard output print $im->png;
# The program implements the function called heapsort.
# This function takes the amino acid letters form the sequence
   and sorts them before ramdamization.
use constant IM => 139968; use constant IA =>   3877; use constant IC =>  29573;
use vars qw(@ra);my $LAST = 42;
sub gen_random { ($_[0] * ($LAST = ($LAST * IA + IC) % IM)) / IM }
sub heapsort ($\@) {my $n = shift;
# use typeglob ra to refer to array.
 local *ra = shift; my($rra, $i, $j); my $l = ($n >> 1) + 1; my $ir = $n;
   while (1) {if ($l > 1) {$rra = $ra[--$l]; } else {$rra = $ra[$ir]; $ra[$ir] = $ra[1]; if (--$ir == 1) {$ra[1] = $rra;
return; }}$i = $l; $j = $l << 1; while ($j <= $ir) {$j++ if (($j < $ir) && ($ra[$j] < $ra[$j+1])); if ($rra < $ra[$j])
{$ra[$i] = $ra[$j]; $j += ($i = $j); } else {
$j = $ir + 1; }}$ra[$i] = $rra; }} my $N = $ARGV[0]; $N = 1 if ($N < 1);
# create an array of N random doubles
my @ary = ();
for (my $i=1; $i<=$N; $i++) {$ary[$i] = gen_random(1.0); }
heapsort($N, @ary);
printf("%.10f\n", $ary[-1]);

#=================================================================
# Program Description: This program implements the graphics utility. This
#                      program was taken form this site the reference to it is
#                      http://biolinx.bios.niu.edu/bios546/gd_mod.htm
#=================================================================
#!/usr/bin/perl -w
# This is a script that demonstrates some of the capabilities of the GD.pm
# graphics module: gd_test.pl
# The script can be run anywhere on biolinx (but you need to modify the path to
# the image file) and the resulting image
# is seen at the bottom of http://biolinx.bios.niu.edu/bios546/gd_mod.htm
use strict; use GD;
# open the image file
open PICFILE, ">image.png" or die "Couldn't open image file: $!\n";
# create new image object
my $im = new GD::Image(760, 420);
# create a set of colors
my $white = $im->colorAllocate(255,255,255);
my $black = $im->colorAllocate(0, 0, 0);
```

```
my $red = $im->colorAllocate(255, 0, 0);
my $blue = $im->colorAllocate(0, 0, 255);
my $green = $im->colorAllocate(50, 200, 0);
my $purple = $im->colorAllocate(200, 0, 255);
my $orange = $im->colorAllocate(255, 200, 0);
# set background and interlacing
$im->transparent($white); $im->interlaced('true');
# draw a border around the image
$im->rectangle(0, 0, 759, 419, $black);
# a horizontal line
$im->line(10, 20, 300, 20, $red);
# a diagonal line
$im->line(10, 20, 30, 40, $orange);
# a small box
$im->rectangle(500, 30, 550, 80, $green);
# a small filled box
$im->filledRectangle(570, 30, 620, 80, $green);
# an arc
$im->arc(100, 100, 50, 80, 90, 270, $black);
 # an arc the other way
$im->arc(300, 100, 50, 80, 270, 90, $black);
 # a shorter arc
$im->arc(200, 100, 80, 80, 0, 45, $black);
# a filled circle
$im->arc(450, 100, 60, 60, 0, 360, $red);
$im->fill(450, 100, $blue);
 # polygon
my $poly = new GD::Polygon;
$poly->addPt(60, 220);
$poly->addPt(80, 280);
$poly->addPt(200, 300);
$im->polygon($poly, $purple);
# some text
$im->string(gdTinyFont, 20, 330, "This is the tiny font", $blue);
$im->string(gdSmallFont, 20, 350, "This is the small font", $purple);
$im->string(gdMediumBoldFont, 20, 370, "This is the medium font", $green);
$im->string(gdLargeFont, 20, 390, "This is the large font", $red);
$im->string(gdGiantFont, 400, 350, "This is the giant font", $orange);
$im->stringUp(gdSmallFont, 250, 400, "This is the small font rotated 90 degrees", $purple);
# print the image as PNG
binmode PICFILE;
print PICFILE $im->png;
close PICFILE;
```

APPENDIX B: INPUT SEQUENCES (mFAST)

Cytochrome Oxidase

>lcl|consensus Cytochrome b-561 / ferric reductase transmembrane domain. Cytochrome b-561 recycles ascorbate for the generation of norepinephrine by dopamine-beta-hydroxylase in the chromaffin vesicles of the adrenal gland. It is a transmembrane heme protein with the two heme groups being bound to conserved histidine residues. A cytochrome b-561 homologue, termed Dcytb, is an iron-regulated ferric reductase in the duodenal mucosa. Other homologues of these are also likely to be ferric reductases. SDR2 is proposed to be important in regulating the metabolism of iron in the onset of neurodegenerative disorders.

----------LHGILMILGFGFLMGEAILVAR-----
WPLTRFLSKPTWFLLHRVLQILALVLGVIGLLAIFISHNESG--------IANFYSLHSWL GLAAF VL A G
LQPLSGFLRPLPPgl--pSSYRSYLNPYHRFVGLAIFILAIVTIFLGL----------

>gi|20875253 RIKEN cDNA 1600010M23 [Mus musculus]

----------MALAF C L CMAEAILLFSp---
eHSLFFFCSRKTRIRLHWAGQTMAILCAVLGLGFIISSKIRSE--------MSH LVS WH
SWIGALTLLATGGQALCGLCLLCPRaa--rVSRVARLKLYHLTCGLVVYLMATVTVLLGMysv
wfqaqikgtawylclglplypalvimhqisssylprkkvei----------

>gi|461668 Putative cytochrome b561 (Cytochrome b-561)

----
msllfdpgfvilredqsvklfniilvmsqvfgglavllvtiwmskfesgfawnedpdkefnYHPTFMIMGMVFLFGEALLVYR
-------VFRNERKKFSKTLHVILHSCVLVFMLMALKAVFDYHNLHKdpsgnpapIVNLVSLHSWIGLSV
VILYFAQYIVGFITYFFPgm--pIPIRQLVMPFHQMFGVLIFIFVSITVAMGIseraawkhtcwtkegQmc aqqa
tssfvgvftflytvcvlllvlnprwkrqslpeeeglhhltsshsmsd----------

>gi|5824381 Hypothetical protein C13B4.1 [Caenorhabditis elegans]

mklqfllvfaliqpsyqqfdasqcqiskgchipestqsngmgvawsllddetlllelfvnsdeekgryvavgfsndehmgnepviecsaignqkpsmkfsfdktn
gkgneriagdytahfsnntavfengvlycksnvkvsgssensnvfkfdpstqyhlllangkttakglgyhkdqssvsrklrlsesspgfdqsecgktkgctmpaans
cynvdgnigasyqvisdnqiafeifgpanttvnenvyvalgfsddekmanisviecsnlpsetaptmkfsynpgfknaridgeppirakfiqqsigrisdgsiyckg
vvnvggeaenpqifkwnknqgyhlmfaagfsadtgltqhwgscvsiltfldqvnnlgfndatcgltkgcftptdctdgcddirsswsllsdnqihveltgkvnatnk
yvamgfstngtmgntsviecssfdnsnfsmtfsynlvnapdysnlrstsdvsglftnrrvqfvdgvlycsadvavvgdandqtvfkydpatkysiimatgdtstkg
nvkglgyhkkkrsvaplqllsdytpptaapppsgkgtfdsstcgkdkacytppnnvdtvaykvlndsyiefeisstqssssgvytalgfsndgkmnpanviecsslg
sqplsmkfstnsgysndrisgeeairsqyitntetsyvdgkiyckgtvrsdgnsnaaifkytpkqqyhliiakgtaspgglgyhgtnryistarlltdlgagnesgssntll
iLHAMFMTIAWMTMVPIAVIFARvlrssPTTKPGGLLIWFHIHRGANLIGIALMIAAFVLILIHKDWKftTIGWGG
KHAIGIIALCLAWLQPFISTLRCSPnDSRRPIFNYIHRGIATAICIAGYHFTGGRHvvqlvlalipisvifalslffiifnnvvdvdt
ksftktngasartedipmrptsktesettwaiqspptstdsnrevpaekkrlwvnrfrefvvygavlifiavgtilsvffgtgfs----------
---

>gi|2832700 unknown protein [Arabidopsis thaliana]

----------mkiskslwsvmisilfyltsappfvicssl
evtidnhspsnlktkgsleqdklshqminsikLHGILLWVSMGFLMPVGILFIRma-nKAHENGIKVKVFFYLHV
IFQILAVVLATIGAILSLRTLE----------NSFDNNHQRLGLALYAAMWLQFLTGVFKPSRG-----
SKRRLRWFLLHWILGTIVSIVGIVNIYTGIqayqkktslsrdsslwtilftvqvtclvffylyqdkwehfqkqrvvldeldhqnnntngrnnqsi
qvvtrndheqkvmvpqpcrksnalicrerereenkmvgeeetkkrvvteslgwltessimpkkhraiegvgpssimelkaqlyksqeeakqtkdftgsdaqyhr
akeriaakdsfaaknsgvesrnlkdklehkavkdgavsyaalekkaqlydklargelsdeegeekycvdffrkgiqhedpkpsstynssisappedfkqdgeddg
slfstkfaglghaigtadvgqhvrmvrevheevnqarekatelkqrrqeqatnrreklkqaylrkqleklkaqqqqqedeqkt----------
---

>gi|1208844 Hypothetical protein M03A1.3 [Caenorhabditis elegans]

----------mlllysilfmcisslraaptcepnsfcyspnestkvtltrtg
dslnlriydensairkvhilqkegkdvlvdctnkkedgktceaqltvdqfeknlpisiklsdsqtsdpislealvppaqegltkqqrrqfskAHAILMIFGWLL
FVPSGFLFARlgkdlFKEQTLFGSAVWFQIHRAANFMGVVCMCTSMLCIFISTQWTWkgt--
gsgSKYWTEVHTDLGVISTVLAVAQPINSLFRCGPT-HSQRIIFNWAHRCVGIVAYTLALTAIIIAAvqf
kriwneplmelvlvclpiaiclaltiaftflesdrfrtkasfgphilkgpavfwaigvffciavalsllvvngyknvnllefvcgfpigssnidvktykletlksenltsceid
fypgdvllmsessslkwsnekseffnfheicnpkieglskefkrllvklhailmilgwlffvptgflfarygrqvfknhtiygmfvwfqihrastfigvccivtsilcilis
tnwtwkgtgseawywtqwhtdfgtistilafsqplnsllrcppsnsqrsifnwahrivgllsytfavaaiyvaaanyrktwseptmeivltsvptilciatgfvvlylese
qrngyrevemiekseknskkperlqliqiswimnrfaillalpllalaatpneklklccatlkdadkecvdrfcdfnalsqanilnfmstcgergptvgemwdcaslr
hnhedcckkagvsgeclkyctahkgapsnyldyafctenfneirdcfynhldknepfkkl

>gi|20197988 expressed protein [Arabidopsis thaliana]

---
matlilsfllllatklpeslaghcttttatksfekcislptqqasiawtyhphnatldlcffgtfispsgwvgwginpdspaqmtgsrvliafpdpnsgqlillpyvldssv
klqkgpllsrpldlvrlssssaslyggkmatirngasvqiyasvklssnntkihhvwnrglyvqgysptihpttstdlssfstfdvtsgfatvnqnsgsralkvTHGV
VNAISWGFLLPAGAVTARLRQMQSIGPTWFYIHAAIQLTGFLLGTIGFSIGIVLGHNSPgVTYGLHRSLGIATF
TAAALQTLALLFRPKTTNKFRRYWKSYHHFVGYACVVMGVVNVFQGFevlregrsyaklgyclclstlvgvcvamevnsw
vvfcrkakeekmkrdgltgvdrcsgshs----------

>gi|7298612 CG13078-PA [Drosophila melanogaster]

---
msddktkptsvlqhiesalyvinqlcigfvtiwiswtclrqdlsgirLHAWLVTFGFVFLMAEGMMCFYd---
gSWLTVRYSRNYKTAFHVVLQILGGGMGVAGCLIQLIRDD----------WSISVTLHARLGFAAFVLC
LISLLSGLVAFLARclsrTISPLVNKTFHVVLSFTAFVIAMMAQFYGYtqtgifrgqgqdfvvlmqvvtmvlmvltsigaikslyqk
igslas---

>gi|7298601 CG10165-PA [Drosophila melanogaster

------maegytkatawlqi hsllnsinhiliflvavfffilarslefkdtaMHMFM
TGTGFHVLIAQAMMSHSk---vNPLTRWLSHRNKSRFHAILQIVGGSMVLLGSLGKFSSKE----------
VHFNTWHGRVGGAASFFCAASIVGGFVNYFQPkfalkVMPPSELRFRHNLFGLVTFSLGMGAIYLGYyskfftky
vdtdfipgmmlitgivygltiiapvssllklkyrskkkaeqaq---

>gi|7290378 CG3592-PA [Drosophila melanogaster]

---
msqgenattaklvfyefawpllvavfevnlyriilellahillivitvvmvkktsgldd hssgQH
ALYAILGLFLCVGESLLVCHs----WWLGDFISENRLNLLHMVLGMVGLWLGLVGIFAKSIFKSKIH--------
EPHFNSKHGLCGLLGFLLIAGAVASGFALVCF--THLALHVIHRLMGLCGFVLLSCSQWFALnlg
farrewsswkikrlristlaatisvvsyeflclcrdivhllpnswfkaiglkidhlhn---
---

Alcohol Dehydrogenase

>lcl|consensus Short-chain alcohol dehydrogenase. This family contains a number of bacterial short-chain alcohol dehydrogenases that are approximately 400 residues long. Alcohol dehydrogenases display a wide variety of substrate specificities, and play an important role in a broad range of physiological processes. Short-chain alcohol dehydrogenases form part of a group of alcohol dehydrogenases that are dependent upon NADP.
----------MIIKPK-VRGFICRT
AHPVGCEANVKEQIAYVKKAGKIKNGPKRVLVIGASSGYGLAARIAAAFGGG-ADTIGVS
FERPGTEKKPGTAGWYNNAAFKKFAEEEGLYAKSINGDAFSDETKTKVIELIKEEFGGKV
DLVIYSLAAPRRKDP-KSG----EVYRSVLKPIGAPVTGRTLDTEKD---QIIETTVEPA

TEEEIADTVKVMGGEDWELWIDALAEAGVLAEGAKTIAFSYIGPEITHPIYWDGTIGRAKKDLDQTAHALN
EKLAA-LGGG-AYVSVLKALVTQASSAIPALPLYLSLLYKVMKEKGTHEGCIEQIYRLFSEK
LYGQDa-RPPVDDEGRLRLDDWELRPDVQAAVEELWPQITPENFKELTDYAGFKKEFLNLFGFGV
DGVDYSQDV----------

>gi|9658208 hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961]
----------MHIKPI-IQGVVARS
AHPYGCEQAVLQQIQYVKQANPIKSGPKRVLILGASSGFGLAARIALTFGGAqADTIGVSFERAPSE
TQTGSAGYYNNLFFKQHAEQAGRIAVNLEGDVFSVDMREQVIEAIETYFEGEVDLIIYSIASGMRRKP-
RSEkadpEFWRSAIKPIGEAVSGATLLLEND---TWIETTLQPASEEEIEGTLRVMGGDDWENWID
TLINAESLAEGCKTIAFSYMGPDVTHPIYLDGTLGRAKIDLHQTSHALNLKLAN-FDGG-AYAVVC
KALVTKASVFIPGLSPYLLALYQVMKNKGTHEGCIEQMQRLFSDKLYGHS—RIPLDSERLIRMDD
WEMNPDTQVQVRERLQQMNASNFQQLGDYAGFKREFMQLNGFEFDQIDYSQSVdmhnfinkk---

>gi|27358280 Uncharacterized paraquat-inducible protein B [Vibrio vulnificus CMCP6]
----------MRIEPI-IQGVVARAHPFGCEAAIKKQIAFVKAPQISQGPKRVLI
LGASSGFGLAARIALTFGGAqADTIGVSFERGPSEKGTGSAGWYNNVFFKREAEKEGRIAINIVGDAFASET
RTQVIEAIETYFEGEVDLVIYSLATGMRPISnQPG----EFWRSVIKPFGQTVTGASFDLEHDR
WIDTTLESATEEEALHTIKVMGGEDWESWIDTLINAESIAQGCQTIAFSYVGPEITHPIYLDGTLGKIDLHQT
SHSLNLKLAN-FDGA-AYATVCKALVTKASVFIPALSPYLLALYRVMKDEKCHEGCIEQM
QRLATKLYGQD--HISVDGERLVRMDDWELAPHIQNKVNQILEEMDANNFQVIGDYQGFKNEFLQ
LNGFGFDEVDYSQDIdlqtilkltp--

>gi|28809171 short-chain alcohol dehydrogenase family [Vibrio parahaemolyticus]
----------MRIEPL-IQGVVARSAHPYGCHASIKEQIEYVKKAPKIKSGPKR
LIIGASSGFGLAARIALTFGGAeADTIGVSFERGPSEKGVGSAGWYNNIFFKQEATHAGRTAINIV
DAFSDSVRNEVIEAIETYFEGEVDLVIYSLAAGVRPKP-HSD----TFWRSVIKPIGESVTGASILLEND-
QWVETTLEPATEEEAEATIKVMGGEDWESWIDTLINTESVAQGCKTIAFSYMGPEVTHPIYLDGTLGRAKI
DLHQTSHALNLKLAN-FDGG-AYATVCKALVTKASVFIPALSPYLLALYRVMKEKGTHERC
IEQMQRLFTTKLYDQP—KVPVDGERLIRIDDLELDPQTQAEVSHLLEQMNTENFKECGDYQGFKD
EFMKLNGFNFDDVDYSQDIsletlaslkp--

>gi|15981993 conserved hypothetical protein [Yersinia pestis CO92]
----------MIIKPR-VRGFICVT
AHPTGCEANVKKQIDYVTTEGPIANGPKRVLVIGASTGYGLAARITAAFGCG-ADTLGVFFERPGE
EGKPGTSGWYNSAAFHKFAAQKGLYAKSINGDAFSDEIKQLTIDAIKQDLG-QVDQVIYSLASPRR
THP-KTG----EVFNSALKPIGNAVNLRGLDTDKE---VIKESVLQPATQSEIDSTVAVMGGEDWQMWI
DALLDAGVLAEGAQTTAFTYLGEKITHDIYWNGSIGAAKKDLDQKVLAIRESLAAHGGGdARVSV
LKAVVTQASSAIPMMPLYLSLLFKVMKEKGTHEGCIEQVYSLYKDSLCg---dSPHMDQEGRLRAD
YKELDPEVQNQVQQLWDQVTNDNIYQLTDFVGYKSEFLNLFGFGIDGVDYDADVnpdvkipnliqg

>gi|24986379 conserved hypothetical protein [Pseudomonas putida KT2440]
----------mAIIHPK-VRGFICTT
THPKGCELNVRDQIEATRKLGVREDGPKKVLVIGASSGYGLAARITAAFGFK-ADTLGVFFEKPGT
ETKAGTAGWYNAAAFDKFAKAEGLYSKSINGDAFSDEARAKVIELIKNEMGGKVDLVIYSLASPVRKLP-
QTG----EVIRSALKPIGQPYKSTAIDTNKD---TIIEASIEPATEQEIADTVTVMGGQDWQLWID
ALAGANVLAEGARTVAFSYIGSDITWPIYWHGALGQAKQDLDETALRLNQKLAGeVKGG-ANVA
VLKSVVTQASSAIPVMPLYLSMVFKIMQEKGVHEGTQDQLDRMYRDRMYRTDgaPAEVDEKGRLRLDDW
ELRDDVQNACKALWPQVTTENLFELTDYAGYKKQFLNLFGFERADVDYDKDVatdvkfdcvel-

>gi|28057027 conserved hypothetical protein [Xylella fastidiosa Temecula1]
----------mdwvvrsitynmlqlqhsqeillLIIHPK-TRGFICTT
THPVGCEYNVLEQIQSTRARGVRSNGPKKVVVIGASSGYGLATRISAAFGFG-ADTLGVFFEKPGT
EKKPGTAGWYNAAAFDKSAKNAGLYSRSINGDAFSDEMRAKVIEIIKSEMGGHVDLVVYSLASPL
RKMP-STG----EIKRSVLKPIGVAHTSNAIDTNKD---QIIQATVEPATEQEIADTVAVMGGQDWELW
INALAQADVLAPQTRTVAFSYIGTEITWPIYWHGALGKAKADLDATSRRLDARLQF-LGGG-ANVA

VLKSVVTQASAAIPALPLYIAIVFKVMKEKGLHEGTIEQADRLLRERLYREDgqPAAIDEEHRLRLD
WELREDVQAACKVIWEQVTNENLFQLTDYANYKRDFLKLFGFERADVDYDADVnpevafdviel-

>gi|18145738 conserved hypothetical protein [Clostridium perfringens str. 13]
----------MIVEPK-FRGFICTT
SHPIGCKKNVENQIEYVKENGKI-EGAKRVLVLGASTGYGLASAIVASEACD-AEVLGVSFEREAK
GKRTASAGWYNIESLKKFVEGEGKKFISVNGDAFSNEVKSEVIDLIKENMG-KVDLVIYSLAAPKR
KDP-VSG----EVYSSCLKTVGAPFTSKTLDFHTG---EIQNITINPATEEEIEGTRKVMGGEDWMLWIE
ALKEANVLENGVKTIAYSYIGPEVTYPIYREGTIGRAKNDLEKTAGEITKVLKS-LNGE-GYISVNKA
LVTQASSAIPIVSLYISILYKVMKEKGTHEGCIEQIYRMFKE-LYEG---NLNLDSENRIRIDDLEMAED
VQKAIEEIWPQITSENVFELSDAEDFKKEFFKLFGFGLEGVDYSEDVdittv-------

>gi|15023320 Protein of short-chain alcohol dehydrogenase family [Clostridium acetobutylicum]
----------MIVKAKfVKGFI-RDVHPYGCRREVLNQIDYCKKAIGF-RGPKK
VLIVGASSGFGLATRISVAFGGPeAHTIGVSYETGATDRRIGTAGWYNNIFFKEFAKKKGLVAKNFI
EDAFSNETKDKVIKYIKDEF-GKIDLFVYSLAAPRRKDY-KTG----NVYTSRIKTILGDFEGPTIDVR
EITLKKVSSASIEEIEETRKVMGGEDWQEWCEELLYEDCFSDKATTIAYSYIGSPRTYKIYREGTIGIAKKDL
EDKAKLINEKLNRvIGGR-AFVSVNKALVTKASAYIPTFPLYAAILYKVMKEKNIHENCIM
QIERMFSEKIYSNE—KIQFDDKGRLRMDDLELRKDVQDEVDRIWSNITPENFKELSDYKGYKKEF
MNLNGFDLDGVDYSKDLdiellrklep--

>gi|15824032 hypothetical protein [Streptomyces avermitilis]
mcvwtprrcstgrhrttwsstssrhcsttdpaeepmmppsmtqseRVVKPT-GRGYLLLD
AHPVGCFRSVELMRAEVPVPEKPPARRPTALVIGSSSGYGLASTIAGLVRYG-IDGVGIGLERPAGH
-RSATAGWYRTVATDAIARELGADFSFRNADAFADTTKTETLDLLAERFG-GVDYLIYSVAAPRRT
DP-RSG----TTYQSVLKPLGAPHTTRNLEFADDgaaQVREVTVAPATEAEAAATVGVMGGEDWSRI
TALAERGLLRSGFRTVALTYIGSPLTSAIYRGGTIGAAKAHLESTARALTERLAA-VDGR-AFTSVN
GALVTQALTAIPGIPLYVSLLRGVLGDR--FPSPVAQSLDLWHQ----LTarRPDVDDSGRIRLDRWELS
PVQAAVAERWRSITPETVTALADTAWFRAQCRALYGFDVPGVDYTVPVatdlpwpes---

Glukokinase

>lcl|consensus Glucokinase [Carbohydrate transport and metabolism]
----------MKAMGYPRLVG-DIGGTNARFALVEIAP--AEPLQA-------ETYACADYPSLEEAVQDYLSE
H--TAVAPRS---ACFAIAGPIDGD-EVRLTNHDWVFSIARMRAELGLDHLSLINDFAAQALAIPRLGA
EDLEQIGGGKPEPN------APRAVLGPGTGLGVAGLVPNGGG-WIPLPGEGGHVDFAPRSEREFQILY
LRAR—FGRVSAERVLSGPGLVNLYRALCAAD----------GRLPEDLTPAAITERALAGGDALARETL
SLFCAILGRVAGDLALTLGARGGVYIAGGIVPRILEALKASGFRARFEDKGRMS-AYLADIPVYVIL
HPQPGLLGAAAALRQP----------

>gi|20138118 Glucokinase (Glucose kinase)
----------MGAMGVNFLAG-DIGGTKTILALVTINE—SSPGLArpvtlfeQTYSSPAFPDLVPMVQQFRQ
EAafVLGNPISvakACFAIAGPVIDN-TCRLTNLDWHLSGDRLAQELAIAQVDLINDFAAVGYGILGL
GSEDLTVLQAAPVDPS------GAIAILGAGTGLGQCYVIPQGQGrYRVFASEGAHGDFAPRSPLEWQL
LEYLKKKysLGRISIERVVSGMGIAMIYEFLRHQYperesaqfsklyqtwNREKDQETKtvdlaAAVSQAALE
GTDVLADQAMELFLGAYGAEAGNLALKLLPRGGLYVAGGIAPKIIPLLEKGSFMQGFSDKGRMQ-
SLMGTIPVQVVLNAKVGLIGAAVCAAQS----------

>gi|17988595 (NC_003318) GLUCOKINASE [Brucella melitensis]
mtgedmqaiidaEQSFKFPVLVG-DIGGTNARFSILVDSN--AEPKEF-------PVLQTADYATIDEAIQHAILD
Q--TAIQPRS---VILAVAGPVDGD-EIDLTNCDWVVRPKKMIADLGFEDVTVLNDFEAQALAVVSLE
GHHMEQIGGKPEEAV------ATRVVLGPGTGLGVAGLVCTRHA-WVPVPGEGGHIDIGPRTERDYQI
FPHIERI--EGRVTGEQILSGRGLRNLYLGICAAD----------KITPTLETPVDITSAGLDGSNPQAAET
LDLFATYLGRLAGDLALIFMAHGGVYLSGGIPVRILSALKAGSFRAAFEDKAPNK-AIMRDIPVRVI
TYQLAALTGLSAFARTPsrfevstegrrwrmrr

>gi|20138130 Glucokinase (Glucose kinase)
----------mdGNHSGGLGLVG-DIGGTNARFALVEFDG--QDPRLIe-----pTAYRGEDYGTAEDAIEEYLR
KVg--VKHPDQ---AVVAVAGPIDHG-QVHMTNLDWRISEDGLRRAGGFRNAKLINDFTAQALAAPR
VGPKDLRQIGELPTSGE------GDLAILGPGTGFGVAGLVRRHGQ-EIPLATEGGHVAFAPVDDVEIEV
LRALTRRldGGRVSVERILSGPGMEDLHVDLAAAE----------GRGVEALTA-----KQITERAVE-GC
ADSLATVNRFCAILGSTAGDIALTLGARGGVFIAGGIAPRIIDILEKSPFRERFDSKGRLS-GFTRSIPT
HVILHPHTALIGAAVALTPEgraavs----------

>gi|20141022 Glucokinase-like protein CC3167
----------MNGRDLALALVSPGD--APRGHR--------DLACASLKALEEHLIDAVSEHs--ADG
LIG---AAVCGAGPEIDG-AIALTAGDFTLTQAWLRAVLKTPRVSLLNDFAACALGAPRLAPSAMRLI
HEGKPGRN------AQIAVIGPNLGLGVAALTPHRTDgWTPVVSEGGHIDFTPGEPREVPVFEALQAR--
HGRVSAEHFLSQQGLADIYAALGGGL----------D-DSDE------VILARVRD-GDETAREALSIFSA
LLGAFAGDAALSFAARGGVYINSPLMERIDGLLDQAAFSRRFEDKGRMS-AYLKDIPVYL
AVGRCTLLGLSALFTASDlryeaaevkvldc---

>gi|20138111 Glucokinase (Glucose kinase)
----------mpKTETYPRLLA-DIGGTNARFGL-EVAP--RQIECI-------EVLRCEDFESLSDAVRFYLSKCK
ESLKLHpiyGSFAVATPIMGD-FVQMTNNHWTFSIETTRQCLTLKKLLVINDFVAQAYAISAMQEND
LAQIGGIKCEIN------APKAILGPGTGLGVSTLIQNSDGsLKVLPGEGGHVSFAPFDDLEILVWQYAR
SK--FNHVSAERFLSGSGLVLIYEALSKRKgle---------kvaKLSKAELTP-----QIISECALNGDYPICRLTL
DTFCSMLGTLAADVALTLGARGGVYLCGGIIPRFIDYFKTSPFRARFETKGRMG-AFLASIPVHVVL
KKTPGLDGAGIALENYllhdki----------

>gi|20138132 Glucokinase (Glucose kinase)
-------mnndnKRSAGGLGLVG-DIGGTNARFAL---WR--GQRLESi------EVLACADYPRPELAVRDYLA
RIgeSVANIDS---VCLACAGPVGAA-DFRFTNNHWVINRAAFREELGLDHLLLVNDFSTMAWAASR
LGADELVQVRAGSAQAD------RARLIIGPGTGLGVGSLLPLGGGrWEVLPCEGGHVDLPVTSPRDF
ALWQGLQAR--YGHVSAERALSGNGLLALYEISCALD----------GVAVRASSa----AEVGALAMA
GDAQADAVLEHFFLWLARVAGNAVLTVGALGGVYITGGIVPRFLERFIASGFAEAFASRGKTsgAY
LQDVPVWVMTAEHPGLLGAGVALQQAldaeg----------

>gi|20138137 Glucokinase (Glucose kinase)
----------MNAPQAPVLVA-DIGGTNARFALANPTL--TSAPLLnd---slREFAVIEFPSLSEAAQHYLHH
Ig---IHTTK---GVFAIAGHVDGD-EARITNHPWVITRTRTATMLGFDTLHLINDFVAQAMAISVLGPQ
DVIQIGSAKWEQVplsaatRNYGIIGPGTGLGVGGLVIRNGR-CYPLETEGGHVSFPPSTPEEIRILEILS
QQ--FGRVSNERLISGPGLVNIHRALSEID----------GIDPGPLRP-----QDITMRAAD-GDIRATRTIN
LFCNIFGAITGDLVLIQGAWDGVFLTGGLVPKLLNSIQHSGFRQKFEHKGRFS-AIMARIPSLAVIHP
HPGLLGAAAYARDTepvpqdika-------

>gi|20140886 Glucokinase-like protein Xf1460
-mlvtsmipnptRDAPNIPSFVAaDVGGTHVRVSVVAAAPtcASPPQLld----vRTYRCADYPSLSTILNDFL
GTR----SAVRD---CVIASAGFQRSDgTVITTNLPWPLSPHRLRADLDLAEVSLVNDFEALAYATEDM
EAAQLLHLTGPAKAQD------GPRLLLGPGTGLGAALWIPNNGR-PIVLPTEAGQAALPSTTELEMQL
VRHMLNN--RTHVPIEHALSGPGILNVYRALCALQ----------SVLPQHASP-----DAISHAAAAGTD
MLSSQTLEVFCDFLGSIVGDLVMMYGAQGGVYLAGGILPQLREPLLRSHFVERFLNKGPMGEALQ
HVPVRLIEHGQLGIVGAARWYLNKkat----------

>gi|20138113 Glucokinase (Glucose kinase)
----------MTLLLAG-DIGGTKTILRLVEISN--SSELHNiy----eESYQSGDFPDLVPMVQQFLVKAn--
-IPSHpekACFAIAGPVVNN-TAKLTNLVWFLDTERLAQELSIPFISLINDFAAVGYGIFGLNKQDLLT
LQAGKHQPE------APIAIIGAGTGLGQGFLIKQGNqYQVFPSEGGHADFAPRNELEFQLLKYLLDKhd
IQRVSVERVVSGQGIVAIYQFLRDRKlatespeiaqvvrtwEQQAGQAEKtvdpgAAIGKAAVQGSDRLSEQALQLFI
DAYGAEAGNLALKLLPYGGLYIAGGIAPKILPLIENSNFLLNFSQKGRMR-PLLAEIPVHI
ILNQQVGLIGAALCAARL----------

Glycerol Kinase

>lcl|consensus Glycerol kinase [Energy production and conversion]
----------MLA--DKYILAIDQGTTSSRAIVFDEDGNIVAIAQREF—TQI--------
---YPQPGWVEHDP----LEIWASVRSVLKEALA-----GIKPGEIAAIGITNQRETTVVWDKETGKPIYN-
AIVWQDRRTADICEELKAD---GYEERIREKTGLVL-------DPYFSATKIKWILDNVPGARERAEKGE
LLFGTIDTWLIWKLTg---GKVHVTDYSNASRTMLFNIHSLEWDDELLELLGIPRS—MLPEVRPS--S
EIYGVTGI----------GFLGAEVPITGVAGDQQAALFGQGCFEPGMAKNTYGTGCFLLMNTGEK
PVRSENG-LLTTIAWGLDG----------KVTYALEGSIFVAGAAVQWLRDGLGLIDDASDSEELAESVE
DNGGVYFVPAFTGLGAPYWDSDARGAIFGLTRGTTKAHIARATLESIAYQTRDVLEAMEKDSGI---
K----------LTRLRVDGGASRNNFLMQFQADILG--VPVERPVVLETTALGAAYLAGLAVG------F
WKDLDELA-----ELWPLDKEFEPGMD----------EEEREELYAGWKKAVKRSLGWRKD----------

>gi|417068 Glycerol kinase (ATP:glycerol 3-phosphotransferase) (Glycerokinase) (GK)
mfpslfrlvvfskryifrssqrlytslkqeqsrmskimedLRSdyVPLIASIDVGTTSSRCILFNRWGQDVSKHQIEYstsask
gkigvsglrrpstaparetpnagdiktsgkpifsaegyaiqetkflkiEELdldfhneptlkFPKPGWVECHPqkllVNVVQCLASSLL
SLQTINservanGLPPYKVICMGIANMRETTILWSRRTGKPIVNyGIVWNDTRTIKIVRDKWQNtsvDRQ
LQLRQKTGLPLl------STYFSCSKLRWFLDNEP----------LCTKAYEENDLMFGTVDTWLIYQLT
k---QKAFVSDVTNASRTGFMNLSTLKYDNELLEFWGIDKNliHMPEIVSS—SQYYGDFGIpdwimeklh
dspktvlrDLVKRNLPIQGCLGDQSASMVGQLAYKPGAAKCTYGTGCFLLYNTGTKKLISQHG-ALTT
LAFWFPHlqeyggqkpelsKPHFALEGSVAVAGAVVQWLRDNLRLIDKSEDVGPIASTVPDSGGVVFVP
AFSGLFAPYWDPDARATIMGMSQFTTASHIARAAVEGVCFQARAILKAMSSDAFGegsKdrdfleeisdV
tyekspLSVLAVDGGMSRSNEVMQIQADILGpcVKVRRSPTAECTALGAAIAANMAFKdvnerpLWKLHDVKkw
vfyNGMEKNEQISPEAHpnlkifrsesdDAERRKHWKYWEVAVERSKGWLKDiegeheqvlenfq

>gi|6686116 Hypothetical sugar kinase AF0866
----------MIGVIDAGTTTIKLAVYDED-KLVAIKKEPV----------
----------VKH----------NPKPGWVEIDA----EDLARKCVSFADTAIDEY----------G-VEV
IAITNQRTTAVLWDGKTGRPVFN-ALGWQDMRANALAEEMNRD----STIRMARTAGMIArgvvkllPT
LKNKRRVKWLITLSRlsirpnhtsvklcwmlrELGEKKEKYDLKAGTVDSWLVYRLTg-----EHLTDYSNAA
ATGLYDSYYLRWSEPILKIVGADEE--MLPKTLES—DRIFGEYRN----------VPVTGVIADQ
SASLYALGCWEEGDIKATNGTGTFVDLNVGEEPQASPGG-LLPLIAWKLKS----------EMRYMMEG
MLFYSGSAVEKLKE-IGIYDDVSKTSEMAFRSKND-DMLLIPSFTGLATPHYVSVP-GLLYGISNAMT
REDIVKALLESIAFRIAEIVEIMRKEFPYe----------TDRIRCDGEMSSNDFFLQRIADVTG—LK
VERGAVLSGTSFGAHLVAGRALG------KWK--KDFC-------MPFDKVFEPSLDLSEKYRRWKRLLEIS
KKLKV----------

>gi|15889199 (NC_003062) AGR_C_3493p [Agrobacterium tumefaciens] [Agrobacterium tumefaciens str. C58 (Cereon)]----------MRAILSIDQGTTNSKAILVSESGELLARGSSPV----------GIt----
------YPQPGWVEQDP----NRIWASVREAISACLAAAps-------dVSVEAIAISNQRESVTIW
DGETGEPLGP-VLSWQCRRTAQDCADLIAK---GQSERVMALTGLPI-------DPMFPGAKMRWLLERA
Pk----------gRK----LRLGTIDSWLIHCFTg---gKVHACDASNAARSQVLDLNRQVWSDELCDLF
GIDIN--ALPDLRDS--SGDFGVTSg----------vPGIKDGTPILAAIGDSHAALFGHGAFNPGDGKTF
GTGSSVMTTLPHFIAPERG--ITTTVAWRLGG----------KPTFAFEGNILVSAASLPWMTDILGLPDV
AALVE-LAATAEP-EGPGFVPAFVGLGAPYWDTNARALFSQINFSTTRAQMARAVTDSIAFQVHDV
FAAMRAQSPSg----------FGRLFVDGGPSQNRFLMQCVADMLE—HPVIQRDAPEASALGAA
YLAGLALG------VWSDLNAIA------ALNSNGNTIATs----------TGESRQRLGIWRDAIARSTLPVTSG
nge---------

>gi|14600618 (NC_000854) Glycerol kinase [Aeropyrum pernix]
----------MLAvgDSLLCSVDVGTSGIRLSLYGEDLGLVARYTEEL----------
----------TL----------YYSGNRVEQDA----LILAANVRDMLGKAARSG----------
CNVVGLSIYRGSVVAWRN--GKPLSD-VITWMDSRGLEEYSKLPLG---ARLVSKSPVLGKAL-------K

PGSPALVMRRLWLNHP----------G-ARIWSIDGFLSDMLTg-----EFTSDPGQAALTGLVSP
YSLKPLSLVIRLLGLRGL--ELPRLRLH—NEPLTRVGG----------VLVGPMVADQQAASIGL
GCLRPGCVKATLGTGLFLDAPVEGKPPLFTGD-LIPVVNLALPG----------RVYYGLEGFAAGVGM
VFDAFAR---VLGGFSVLEEKALEPADP--APVVPVLAGLRTPYRPLLR-GAVLGVSPGFTAASLAKG
LIIGTLLTVLSIYRELARRMGG----------FGELRIGGGLSRLGLLASSIASAVG--VKVYRSVD
YNDSARGAALVAGYASDlisreeLLNPPVSLV-----EVEPLEELSLSGVDawl-----glvDALASEDFSRRLE
EIRRSSFRR----------

>gi|15596684 (NC_002516) probable carbohydrate kinase [Pseudomonas aeruginosa PA01]
----------MRIAALDQGTTSTRVLVASQDGSADIQLALRH----------
----------QQH----------HPQSGWVEHDP----LELLANLQRCLEAS----------GRVD
AIGLANQGESCMAWDARSGEPLSP-LIVWQDNRTTPHIERLRAS---GAEALVLERSGLPL-------DAY
FSASKLGWIVEHLP----------AARRALKAGRLRLGTSDAWFLDRLCg-----TFATDVTTASRTAL
MNLAEGRWDPDLCALFGVPIE--CLPEIRDT--VGHFGVIG----------N-TPLTASVVDQQASL
YGHGCRQPGDAKITFGTGAFALTLSGERIIRSPETgLLATIAWQIDG----------KPVYAMDGGVYDA
SAAVEWAGR-LGLFSDFSELAGFDRPPAIERGLAFVPALSGLACPHWDRSAGAMWLGMDAGTRR
EDLCQALLEGVVLRSAEVIQAMDGYLKV----------TDRLSIDGGLARSPYFAQFLADSLQ—
RRIVTQRFDELTAFGCAALAARGLG----------HELA-----EPRNTRTEFQPRVDAGTARRWQVRFSEA
VARTRGWR----------

>gi|6685472 Glycerol kinase 1 (ATP:glycerol 3-phosphotransferase 1) (Glycerokinase 1) (GK 1)
----------MYVLAIDQSTSGTKAIIFDEKGGIVHRVTVYH----------
----------KQY----------YPKPGWVEHDP----EEIFRNTLDACRKVIEES------GIKPLEI
EALAITNQRETTILWEKKSGKPVYN-AVVWQCQRGASLCEEIKKRg---lEGKIKEKTGLVV-------DP
YFSASKIRWILDNVE----------GVKNKAKQGEIAFGTVDSWLIWKLTk---GEVHATDFSNASRT
LLLNIHELRWDEEVLEIFE-IPPeiLPELKSS---DSVFGYTDLg----------FLPKKIPIVGVMGDSSAA
LFGQGGFYSGDIKVTYGTGSSTMLNIGEKPNVSDSP-IVCSVGWVVKE----------TSSYVLEGNIHSA
GDTIVWLKEKLGIISDPSETEKIALSLENNGGVYLVPAFVGLGAPYWRSDVKAAILGLQRNHGKEHVVRAA
LESIAYQVRDIFEEMVRISSKe----------PTEVRADGGITRNRFLMQFQADILN—IPVL
VSNIEEVSARGVAFVALLHLG------AFSDLEEi-----rQKITYREKYEPRMGDELREMYYEGWKTAIR
KLLTE----------

>gi|13541972 (NC_002689) Glycerol kinase [Thermoplasma volcanium]
----------marRPIdsDDIFLALDAGTTDVKAGAYDRSMNLIASCKRRIg----------
----------VY----------YGQGGVVEQDP----HEILEAAKYCLNSILRRIp------KRY
GEPKAIGITNQRESVLAWEPIDGRPITK-LISWKDKRGAQLSLDLKER----YGQVIKDKTGLIS-------D
PYFSATKIKWLVENIK----------RSSNHKNYVITTLDSWLVKNLNsssIKPLTDHSNASRTMLF
NIDSLEWDSDLLEIVGISEE--ILPEVKRTieSDSYGKVKLt----------yGSTTREVPILSVAGDQQASL
FGNGCLYPGQAKASYGTGAFILENTGVR-VKSDR--LLETLFYTYKG----------KRTYALEGTILSSG
SSIDWLVS-LAGLKSVPRSILRAEQIERS-HVLSVPALSGLGSPFYSSDIRGYISGLSESTDIYEVIRSFL
EAQAFLSTVIIEEMRKHIKL----------LEPLHIDGGLSKSDLIAEMLANLLD—MKIIRERNV
DATMKGIAMMSMIGYY--------G-IDERKl----TVSAGGKEFNPNDK------RDEIAEKFNSWRSFLLSVI
SKNQG----------

>gi|16082118 (NC_002578) probable glycerol kinase [Thermoplasma acidophilum]
----------MDANGRIVSFAYRLN----------
-------RQY----------FPAPGWVEQDP----VNLWRNVRITLKKAIEES------RIDLTGIASGVTNQ
RETVLVWDRKTGRPLYN-AIVWQDKRTSRRIKDLDEEt----sNSIMKTTGLRP-------DSYFSASKIQW
LLENVE----------GLRKKMADGDVSFGTVDSWIIWNLNgsvnRSITVTDHSNASRTMLYDIAKL
RWNPDLLDIFGGISEtsLPEVMSSG--SAEYGYISKdt----------saIFDGREVPITADIGDQQSALGQG
CFNPGDVKATYGTGTFILSNAGTEVPQTSGT-LLRTIFYSISGr----------SYALEGSILASGSVLRWLQ
NSLHLFRSAKDIEDAAEKLKSNDGVYFVPAFSGLGSPYWDQDARGLFIGLTESTTADHLARSVLES
EVYMATDVIMEIEKEIGRn----------IAKIRCDGGGSRSDFLMQFQADIAN—AEVLVPESSET
TALGSAYLSGLVSG------LWKSKDEi-----rELWRLKKVYRPVMS----------EEERKRNYVGWKDAVK
RCMGWHPNi----------

>gi|16123465 (NC_003143) glycerol kinase [Yersinia pestis]
----------msTPIILAIDEGTTNAK
AIAVDRAGRVLAKASVPL----------QLe----------HPQPGWAEQDP
----LAIWLAVSQAVEGCLNQLa--------gAQVAGIAISNQRESVLIWERETGTPLTP-VVSWQCRRSEAF
CLALRQL---PAAAMVAERTGLQI-------DPLFPAAKIHGMLAQIPhg----------aERAAHGELCVG
TLDCWLTWQFSe---gQSFSTDFSNAARTQLFNIHSGQWDPDLLALFGIPSL--CLPAVLPS—ASIHGH
TARtg----------iLGLEQGVPIVAHIGDSHAALYGQGGDQAGEIKATYGTGSSLMMTLKQASAPSH
G--LSTTIAWHDG----------ELRYALEGNITHTGSGVAWVSRMLGISDLSRLTD-MAESQSGNQGV
YFVPALSGLGAPYWDSQARGLFCGLTDATTPAVLARAALESVAYQIADVFFAMENAAHHr----------
LERLRVDGGATSNRWLMQFQADLLQ--RTLIRNHTAEVSALGAAYLGGKTLG-----WWQD
SQQLA------ALPREVEYIEPRIh----------SAEMQDNYSLWQTAIARARFQPK----------

Ascorbate Peroxidase

>lcl|consensus Ascorbate peroxidases. This is a subgroup of heme-dependent peroxidases of the plant superfamily that share a heme prosthetic group and catalyze a multistep oxidative reaction involving hydrogen peroxide as the electron acceptor. Along with related catalase- peroxidases, ascorbate peroxidases belong class I of the plant superfamily. Ascorbate peroxidases are found in the chloroplasts and/or cytosol of algae and plants, where they have been shown to control the concentration of lethal hydrogen peroxide molecules. The yeast cytochrome c peroxidase is a divergent member of the family. It forms a complex with cytochrome c to catalyze the reduction of hydrogen peroxide to water.
----------AAPVVDARYLKDLEKARRELALLIAE-------
KGCAPILVRLAWHDAGTYDKTT----KTGGP-NGSIRFKkeLNHGANAGLQIAVKLLEPIKKKFPWVS
YADLFQLAGVTAVEVTGGPKIPFRPGRVDTPEpt-tpDEGRLPDADKG----------AGHLRRVFYR
GLSDRDIVALSGAHTLGRAHKERSGFEGPWTk----------nPLKFDNSYFVELLNG
w----------SGLLKLPTDKALLQDpVFRPLVEKYAaDEDAFFADYAEAHKKLSELGFTFP----------
----

>gi|1420981|pdb|1APX|A Chain A,
----------gkSYPTVSPDYQKAIEKAKRKLRGFIAE-------
KKCAPLILRLAWHSAGTFDSKT----KTGGP-FGTIKHQaeLAHGANNGLDIAVRLLPIKEQFPIVSYA
YQLAGVVAVEITGGPEVPFHPGREDKPEp---pPEGRLPDATKG----------SDHLRDVFkAMGLS
DQDIVALSGGHTIGAAHKERSGFEGPWTs----------nPLIFDNSYFTELLTGEk----------
DGLLQLPSDKALLTDsVFRPLVEKYAaDEDVFFADYAEAHLKLSELGFAEA----------
----

>gi|728873 L-ascorbate peroxidase, cytosolic (AP).

---------mtkNYPTVSEDYKKAVEKCRRKLRGLIAE-------KNCAPIMVRLAWHSAGTFDCQS----RTGG
P-FGTMRFDaeQAHGANSGIHIALRLLDPIREQFPTISFADFHQLAGVVAVEVTGGPDIPFHPGREDK
PQp---pPEGRLPDATKG----------CDHLRDVFAkQMGLSDKDIVALSGAHTLGRCHKDRSGEG
AWTs----------nPLIFDNSYFKELLSGEk----------EGLLQLVSDKALLDDpVFRP
LVEKYAaDEDAFFADYAEAHMKLSELGFADA----------

>gi|1321627 thylakoid-bound ascorbate peroxidase [Cucurbita cv. Kurokawa Amakuri]
maatalgsvaassasttrflstatratlpfssrssslssfkflrsaplishlflnqgrpsscvsirrfnaaSHPKCLASDPEQLKSAREDIKELLKT-------
TFCHPILVRLGWHDAGTYNKNIeewpQRGGA-NGSLRFDveLGHGANAGLVNALKLIEPIK
KKYSNVTYADLFQLASATAIEEAGGPKIPMKYGRVDVVGpeqcpEEGRLPDAGPPs----------pAA
HLREVFY-RMGLNDREIVALSGAHTLGRSRPERSGWGKPETkytkdgpga----------pggqswtvqWL
KFNNSYFKDIKERRd----------EELLVLPTDAALFEDpSFKVYAEKYVeDQEAFFKDYAEHAKLS
NLGAKFDppegividdasskpagekfdaakysygkrelsdsmkqkiraeyesfggspdkplptnyflniilviavlailtsllgn

>gi|2887338 Chlamydomonas reinhardtii mRNA for ascorbate peroxidase, complete CDS, and translated products
----------mqsarvsrtarhtrpscrpqravAVRVSAKVNVEQLKALKAELYNYIN

S-------RGCNPISVRLGWHDSGTYDKNIaefpARGGA-NGSIRFKpeIDHGANKGLAIALAILNPIKKKY
PDVSYADLFQMASATAIEASGGPKIPMRYGRKDAKGpeecsPDGRLPGAAHPfadg----------sgspAEHL
RMGLNDQDIVVLSGGHTLGRARPERSGFGAEKTkytdvgpgtstaspsgat]drpvtpkpvgqqgtswtvnWLEFDNACIFED
dQFRPYAEKYAaDQAAFFADYCVSHQKLSELGVEWEegapvtld----------

>gi|3377755 ascorbate peroxidase [Mesembryanthemum crystallinum]
----------maCGPVVDQRYLKDLEGARRDLASIIQR-------
KNAAPVLLRLAFHDAANYNVTN----NTGGV-NGSVRLRqeLSQPPNKGIEDGVKFCEEVKKKHPR
TYADIIQLAGVLAVELSGGPCIDFVPGRMDTNVa----DKLNIPNPRGG----------ADHLRRTFQM
GLSDKDIVVLSGAHTLGRARKENSGFNGPFTr----------nTLKFDNSYFVLMRGEt
----------PGLVKFPTDKALVQDpVFRPLVELYArHEGAFFRDYAESHKKLSELGFTPSlhvwrwm----------
---

>gi|3377753 ascorbate peroxidase [Mesembryanthemum crystallinum]
----------mAAPKVDADYLKHIEGARKELRTIIST-------
KQCAPLMLRLSFHDAGTYDAKT----KKGGP-NGTVRFE—LNNPANNGIKTAVDLVEQVKVKHPK
VTYADLYQLAGVVAVEVTGGPVINFVPGRPDVQQv----DSGSLPLPSGD----------A\HLREVF
H-RMGLSDRDIVVLSGAHTLGRANRDRSGVDGPFTk----------nPLKFDNSYYVEL
LKGDt----------PELVKFNTDKVLLQDpTFRKYVQLYAkDEKAFLTHYAESHKKMSELGKPKHm----------
---

>gi|3891683|pdb|1BEQ Interaction Between Proximal And Distals Regions Of Cytochrome C Peroxidase
----------lvhVASVEKGRSYEDFQKVYNAIALKLREddeydnyIGYGPVLVRLAWHIS
NTGGSyGGTYRFKkeFNDPSNAGLQNGFKFLEPIHKEFPWISSGDLFSLGGVTAVQEMQGPKIPWRCGRVDT
PEdt-tpDNGRLPDADKD----------AGYVRTFFQ-RLNMNDREVVALMGAHALGKTLK
NSGYEGPYGa----------aNNVFTNEFYLNLLNEDWklekndanneqwdskSGYMMLPT
DYSLIQDpKYLSIVKEYAnDQDKFFKDFSKAFEKLLEDGITFPkdapspfifktleeqgl----------
---

>gi|20151105|pdb|1KXN|A Chain A, Crystal Structure Of Cytochrome C Peroxidase With A Proposed Electron Transfer Pathway Excised To Form A Ligand Binding Channel.
----------lvhVASVEKGRSYEDFQKVYNAIALKLREddeydnyIGYGPVLVRLAWHIS
NTGGSyGGTYRFKkeFNDPSNAGLQNGFKFLEPIHKEFPWISSGDLFSLGGVTAVQEMQGPKIPWRCGRVDT
PEdt-tpDNGRLPDADKD----------AGYVRTFFQ-RLNMNDREVVALMGAHALGKTHL
KNSGYEGGGA----------NNVFTNEFYLNLLNEDwklekndanneqwdskSGYMMLPTD
YSLIQDpKYLSIVKEYAnDQDKFFKDFSKAFEKLLENGITFPkdapspfifktleeqgl----------
---

>gi|5804780
----------migskinaprasmasraaa
plraaarpvrrlAVAPMAKASAATLAECQAECAALVKK-------ASCAPILVRLAWHDSGNYDATT----KTG
NGSIRFDpeMKHGGNAGLPLAVKLLEPIKKKFPDVGYADLFQMASATAIEVSGGPKIDMKYGRVDAADesav
pPEGRLPSAGAPfqeaqgpepakeakdqspQGHLRRVFGRMGLSDQDIVALSGAHTLGRAFKNS
GAAPLEStkftkdgpgt----------kggqswteeWLKFDNRYFTMLLEAEagt----------cdPELLQLATDNA
LLTDpAFRPLVEKYAkDNAAFCADYAAAHKRLSELGSTFE----------

Glyceraldehyde-3-phosphate Dehydrogenase

>lcl|consensus Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain. GAPDH is a tetrameric NAD-binding enzyme involved in glycolysis and glyconeogenesis. C-terminal domain is a mixed alpha/antiparallel beta fold.

TTNCLAPLAKVLN-DNFGIEKGLMTTVHAYTADQKLVDGPHH-KDLRRGRAAA—PNIIPT
STGAAKAVGLVLPELNGKLTGMAFRVPTPNVSVVDLTVELEKPVTVEEINAALKEAAE----GALKG
ILGYTEDPLVSSDFIGDPH--SSIFDAKATIVLN----DNFVKLVAWY----------

>gi|1311021|pdb|1GYP|C Chain C, Chain C, Mol_id: 1; Molecule: Glyceraldehyde-3-Phosphate Dehydrogenase; Chain: A, B, C, D; Synonym: Gapdh; Ec: 1.2.1.12; Engineered: Yes; Heterogen: Nad; Heterogen: Phosphate
----------apikvgingfgrigrmvfqa
icdqgligteidvvavvdmstnaeyfayqmkhdtvhgrpkytveavksspsvetadvlvvnghrikcvkaqrnpadlpwgklgvdyviestglftk
aeghikggakkvvisapasggaktivmgvnqheyspashhvvsnascTTNCLAPIVHVLTkENFGIETGLMTTIHSYTATQ
KTVDGVSL-KDWRGGRAAA—VNIIPSTTGAAKAVGMVIPSTKGKLTGMSFRVPTPDVSVVDLTFR
ATRDTSIQEIDKAIKKAAQ----TYMKGILGFTDEELVSADFINDNR—SSVYDSKATLQNNlpgeKRFF
KVVSWYdnewayshrvvdlvrymaakdaass----------

>gi|6435783|pdb|1B7G|O Chain O, Chain O, Glyceraldehyde 3-Phosphate Dehydrogenase
----
mvnvavngygtigkrvadaiikqpdmklvgvaktspnyeafiahrrgiriyvpqqsikkfeesgipvagtvedliktsdivvdttpngvgaqykpiylqlqrnaifq
ggekaevadisfsalcnynealgkkyirvvscNTTALLRTICTVN-KVSKVEKVRATIVRRAADQ----------K
EVKKGPINSlvPDPATVPSHHAKDVNSVIR—NLDIATMAVIAPTTLMHMHFINITLKDKVEKKDILS
LENTPRivliSSKYDAEATAELVEVARDLKRDRNdiPEVMIFSDSIYVKDDEVMLMYAVhqesivvpenidairasmkl
msaedsmritneslglkgyli----------

>gi|3122122 Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase)
----
misvaingygtigkrvadavaaqddmkvagvsktkpdfearvaiekgydlyvsipereklfgeagipvsgtvedmleeadivvdatpegigaknlemyrekgik
aifqggekhdaiglsfnsfanydeslgadytrvvscNTTGLCRTLKPID-DLCGIKKVRAVMVRRGA
DP----------VQVKKGPINAivPNPPTVPSHHGPDLKTVMK--GVNIHTVALLVPTTL
MHQHNIMVELEDPVEADEIKARLDETTRvmlvRASEGLASTAEIMEYAKELGRSRNdlFE
IPVWEESINVV----DGELFYMQAVhqesdavpesvdairalleleednmksimktnram
gil----------

>gi|120706 Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase)
----
mkikvgingygtigkrvayavtkqddmeligvtktkpdfeayrakelgipvyaaseeflprfekagfevegtlndllekvdiivdatpggmgeknkqlyekagvk
aifqggeaevaqvsfvaqanyeaalgkdyvrvvscNTTGLVRTLNAIK-DYVDY--VYAVMIRRAADP--------
NIKRGPINAikPS-VTIPSHHGPDVQTVIP---INIETSAFVVPTTIMHVHSIMVELKKPLDVIDIFE
NTTRvllfEKEKGFESTAQLIEFARDLHREWNnlYEIAVWKESINVK----GNRLFYIQAVhqesdviPenid
airameiaekwesikktnkslg----------

>gi|3122123 Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase)
----
mmkvkvaingygtigkrvadavslqddmevvgvtktrpdfeaklgakryplyvakpenvelferagieiqgtiedllpkadivvdcspnkvgaenkakyyeka
gikaifqggekkdvaevsfnalanydeavgksyvrvvscNTTGLTRLIYMLK-TNFSIGRIRATMLRRVVDP------
KEDKKGLVNGimPDPVAIPSHHGPDVKTVLPD—VDIVTTAFKLPTTLMHVHSLCVEMREAVKAE
DVVSALSEEPRimliSAEDGFTSTAKVIEFARELRLRYDl-YENIVWRESIGVD----GNDLFVTQAVHqE
aivvpenidairamfelaekeesirktneslgigkvf----------

>gi|3170587 glyceraldehyde-3-phosphate dehydrogenase homolog [Streptomyces roseofulvus]
mipvigrlqrqrdvtvllhsrslvnksvvgilkthrfarqiageelsvtetmpflqalttldlgpsqidigmlaetyksddrglgvaeftarpvegatgerkieraaprdvv
lygfgrigrllarlliekagsgnglrlravvvrktagqdlvkrasllrrdsvhgqfqgtiivdeendtliangnairfiysddpatvdytaygindailvdntgrwrdragls
qhlrpgvakvvltapgkgdvpnivhgvnhetikpderiiscascTTNAIVPPLKAMA-DEFGVESGHVET
VHSFTNDQNLLDNYH--KSDRRGRSAP—LNMVLTETGAASAVAKALPDLGAKISGSSIRVPVPDVS

IAILNLRLSRGTSREEVLTHLREVSLt--sPLRRQIDFTTSADAVSSDFVGSRH—ASIVDAGATKVDG-----
DNAILYLWYdnefgyscqvvrvvqhvsgveyptfpaplg----------

>gi|2494645 Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)
----------mkifingf
grigrcvlrailerndtnpklevigindpanweilayllehdsvhgllpkevrysnykliigsleipvfnsikdlkgvdviiecsgkflepktlenylllga
vllsapfmgeydekqyptlvygvnhfcyqnqaivsnascTTNAIAPICAILD-KAFKIKEGMLTTIHSYTSDQKLIDLAH
P-LDKRRSRAAA—SNIIPTTTKAALALHKVLPNLKNKMHGHSVRVPSLDVSMIDLSLFLEKKAPKD
PINDLLIEASK----GVLKGVLEIDLKERVSSDFISNPH--SVIIAPDLTFTL-----ENMVKIMGWYDnewgY
snrlvdmaqfmyhy----------

>gi|1663533 glyceraldehyde 3-phosphate dehydrogenase
----------msapkldfyhrkvrigisgfgrigrfalryaltcpnvei
aainnrnmerayfhylfthdsvhgpphgftcslscpcgetdcncsgnnsadhnliwfndkpvylftagvaseipwevakvdvvlectgayltvescmqhmsrpn
ttvkkvvisapskektcptfvygvnhkkinagnhtkysvisnascTTNCLAPLAKVIH-ENFGIKQALMSTIHAVT
ATQPVTDSVMKkRDWRSGRACL—SNIIPASTGAASALTLVIPELAGRITGTSWRVPVQDVSVVDL
VVETEKDTSYAEICAAVKRACEt--pDELCGIMAYRDDFCVSSDFLTTTT—ISNFDSKSGIELH---SRF
FKLVSWYdnecgysaklvdmaaylgsfvvmdewaaiektkgrgrtssvlgrdvedvvgssk

>gi|13431512 Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)
----------mtvkigingfgri
grlafrrimdlgeetkdievvaindlttpamlahllkydsthgtfdhevsatedslvvdgkkyrvyaepqaqnipwvkndgvdfvlectgfytskaksqahldagak
rvlisapagndlktivysvnqdtltaddtivsagscTTNSLAPMANALN-KEFGIQVGTMTTIHAYTATQKVL
DGPDRgNNFRNARAAA—ENIIPHSTGAAKAIGLVLPELNGKLDGHAQRVPVKDGSETELVTILDK
KVTAEEVNAAMKKYE--------SPSFAYNADQIVSTDVLGMTA--GSIFDPTQTQVITag-dKQLVKTVA
WYdneysftcqmvrtllhfatl----------

Lactate Dehydrogenase

>lcl|consensus Malate/L-lactate dehydrogenase. This family consists of bacterial and archaeal Malate/L-lactate dehydrogenase. L-lactate dehydrogenase, EC:1.1.1.27, catalyses the reaction (S)-lactate + NAD(+) <=> pyruvate + NADH. Malate dehydrogenase, EC:1.1.1.37 and EC:1.1.1.82, catalyses the reactions: (S)-malate + NAD(+) <=> oxaloacetate + NADH, and (S)-malate + NADP(+) <=> oxaloacetate + NADPH respectively.
----------MRISAEELKSLIKRVLTQAGVPEEDAKIVADVLVDADLRGVHSHGIGRFPRYVQRLSQGG
INPNAQPKIVEEGPATAQLDGDRAFGQVVAKKAMDLAIEKAKQHGVGVVALRNSNHWGRAGYYVQQAA
EAGMIGISMTNSD--PMVAPFGGREPILGTNPLAIAFPGKDK-PFLLDMATSAIAFGKLLVAR
RKGKSIPEGWAVDKEGNPTTDPAVVEKGRR--LLPFG--GHKGYGLSIMIDILSGLLSGGAFGTQVTG
EGCNLGQLFIAINPEFFIDGEEFRAKLDAFMDEVKSSEPADEFERVLLPGEIETLTLRERRKNGIPIDDSVWEK
LKSI----------

>gi|7387868 Malate dehydrogenase
mfekgyvdenyIRVPKDRLFSFIVRVLTKLGVPEEDAKIVADNLVMADLRGVESHGVQRLKRYVDGIISGGVNL
HPKIRVIREGPSYALIDGDEGLGQVVGYRSMKLAIKKAKDTGIGIVIARNSNHYGIAGYYALMAAEEGMIGI
SMTNSR--PLVAPTGGIERILGTNPIALAAPTKDK-PFLLDMATSVVPIGKLEVYRR
KGKDIPEGWAINREGNITTKVEEVFNGGA—LLPLGgfgellgGHKGYGLSLMVDILSGILSGTWSYVK
NTSE--KGSNVCHFFMVIDIEHFIPLEEFKEKISQMIEEIKSSRKHPEFERIWIHGEKGFLTMETRLKLG
IPIYRKVLEELNEIakrvgvegl----------

>gi|17366164 L-sulfolactate dehydrogenase ((R)-sulfolactate dehydrogenase)
----------MRISPEEEVKIIKEILTAMNVPEESSDIVADVTLDADLKGFSSHGIGRFPQYVDGLRHGTIR
ADGDITIERETESTALINGNHIFGHVVAYRAMELAIEKARNTGVGLVGVHDSNHFGVAGYYSDMAVMND
MIGVVIANTE--PAVAPIGGRKPILGTNPVAIGIPSNRY-YVSVDMATSASARGKLLEAARKG
ESIPENVALDAEGKPTTDPEMALKG-S--ILPFG------GHKGYALSFMIEILAGPLVGAAFGTAVTGTN
p-eEMCTKGDLMMAIDPSKMVDPDEFRAQVDEFIEEVKSSG------DVLIPGDIESMNIKRRRAEGIEL
DEKLLERILGIareldinleikel-------

>gi|2497860 L-sulfolactate dehydrogenase ((R)-sulfolactate dehydrogenase) ((R)-2-hydroxyacid dehydrogenase)
----------MILKPENEKKLIIDVLKKFGVPEEDAKITADVFVDADLKGFTSHGIGRFPQYITALKLGNIN
PKPDIKIVKESPATAVIDGDLGLGQVVGKKAMELAIKKAKNVGVGVVATRNANHFGIAGYYSELA
MNQDMIGITITNTE—PAMAPFGGKEKILGTNPIAIAFKGNKY-KFSLDMATASIARGKILEALRKKI
KIPEGCAVDKDGKPTTDPAKALEG-C--ILPFG-------GPKGYGLALAIEMLS-AIGGAEVGTKVKGTA
Np-eERCTKGDLFIAINPEFFMGKEEFKRKVDELLDEIKNSEPA-EGFEILIPGEIEERN-KMKRKDGFE
IDKNLYNQLKEIcnelglniedyie-------

>gi|17367959 Hypothetical oxidoreductase yjmC
--------mktITIAAEEAKELVWQKLDGAGLNERDAEKVADVLVHADLRNVHSHGVLHTEHYVNRLA
GGINPGAQPVFKETGPVTGVLDGDDGFGHVNCDMAMDHAIDMAKKKGVGMVTAVNSSHCGALSFVQKA
ADEKLIGMAMTHTD--SIVVPFGGRTPILGTNPIAYGVPAKHKkPFILDMATSKVAFGKILQ
AREEGKEIPEGWGVDENGEAVTDPDKVVSL----ST-FG-------GPKGYGLSIVVDVFSGLLAGAAFGP
HIAKMYNgldQKRKLGHYVCAINPSFFTDWDTFLEQMDAMIDELQQSPPAVGFERVYVPGEIEQLHEERNK
KNGISIARSVYEFLKSR----------

>gi|2497861 Ureidoglycolate dehydrogenase
----------MKISRETLHQLIENKLCQAGLKREHAATVAEVLVYADARGIHSHGAVRVEYYAERISKG
GTNREPEFRLEETGPCSAILHADNAAGQVAAKMGMEHAIKTAQQNGVAVVGISRMGHSGAISYF
VQQAARAGFIGISMCQSD—PMVVPFGGAEIYYGTNPLAFAAPGEGDeILTFDMATTVQAWGKVL
DARSRNMSIPDTWAVDKNGVPTTDPFAVHAL-----LPAA-------GPKGYGLMMMIDVLSGVLLGLPF
GRQVSSMYDdlhAGRNLGQLHIVINPNFFSSSELFRQHLSQTMRELNAITPAPGFNQVYYPGQDQDIKQRKA
AVEGIEIVDDIYQYLISDalyntsyetknpfaq-----

>gi|2506851 Hypothetical oxidoreductase ybiC
-------mesgHRFDAQTLHSFIQAVFRQMGSEEQEAKLVADHLIAANLAGHDSHGIGMPSYVRSWSQG
HLQINHHAKTVKEAGAAVTLDGDRAFGQVAAHEAMALGIEKAHQHGIAAVALHNSHHIGRIGWAEQCAA
AGFVSIHFVSVVgiPMVAPFHGRDSRFGTNPFCVVFPRKDNfPLLLDYATSAIAFGKTRVAWHKGVPVPPGC
LIDVNGVPTTNPAVMQESPLgsLLTFA-------EHKGYALAAMCEILGGALSGGKTT
HQETLQTSp--DAILNCMTTIIINPELF-GAPDCNAQTEAFAEWVKASP-HDDDKPILLPGEWEVNTRR
ERQKQGIPLDAGSWQAICDAarqigmpeetlqafcqqlas

>gi|1176297 Hypothetical oxidoreductase HI1031
----------MRVSYDELKNEFKRVLLDRQLTEELAEECATAFTDTTQAGAYSHGINRFPRFIQQLEQGD
IVPNAIPTKVLSLGSIEQWDAHQAIGNLTAKKMMDRAIELASQHGVGVIALRNANHWMRGGSYGWQAAE
KGYIGICWTNAL--AVMPPWGAKECRIGTNPLIIAVPTTP--ITMVDMSCSMYSYGMLEVHR
LAGRQTFVDAGFDDEGNLTRDPSIVEKNRR--LLPMG-----FWKGSGLSIVLDMIATLLSNGESTVAV
QVFIAIEVDRLIDGKSKDEKLNRIMDYVKTAERSDPTQAVRLPGHEFTTILSDNQTNGIPVDERVWAKLKTL

>gi|2506852 Hypothetical oxidoreductase yiaK
----------MKVTFEQLKAAFNRVLISRGVDSETADACAEMFARTTESGVYSHGVNRFPRFIQQLENG
DIIPDAQPKRITSLGAIEQWDAQRSIGNLTAKKMMDRAIELAADHGIGLVALRNANHWMRGGSY
GWQAAEKGYIGICWTNSI--AVMPPWGAKECRIGTNPLIVAIPS--ITMVDMSMSMFSYGMLEVNRL
AGRQLPVDGGFDDEGNLTKEPGVIEKNRR--ILPMG-------YWKGSGMSIVLDMIATLLSDGASVAE
VTQDNSd--EYGIS-QIFIAIEVDKLIDGPTRDAKLQRIMDYVTSAERADENQAIRLPGHEFTTLLAEN
RRNGITVDDSVWAKIQAL----------

Plant Peroxidase

>lcl|consensus Plant peroxidase superfamily. Along with animal peroxidases, these enzymes belong to a group of heme-dependent peroxidases containing a heme prosthetic group (ferriprotoporphyrin IX), which catalyzes a multistep oxidative reaction involving hydrogen peroxide as the electron acceptor. The plant peroxidase superfamily is comprised of three structurally and functionally divergent groups. They are found in all living kingdoms and carry

out a variety of biosynthetic and degradative functions. Class I includes intracellular peroxidases present in fungi, plants, and archaeal and bacterial enzymes, called catalase-peroxidases, that can exhibit both catalase and broad-spectrum peroxidase activities depending on the steady-state concentration of hydrogen peroxide. Catalase-peroxidases are typically comprised of two homologous domains that probably arose via a single gene duplication event. Class II includes ligninase and other extracellular fungal peroxidases, while class III is comprised of classic extracellular plant peroxidases, like horseradish peroxidase.

----------AESIVRSDVQEAlks--------dprIAASLLRLHFH
DCFVy----------GC-DGSILLddtg---sekNAPPNagllrGFEVIDPIKAALekac-pgvVSCADILALAARDAV
LAg-gPTWEVPLGRRDSrtssps----------eangnlPSPFDt---------VTQLIAKFARKGl-DVKDLV
ALSGAHTiGRAHCvsfgdrlynftgtgdpdptldpt--------llgkccpsdgdgstlvglddstPTVFDNSYYKNLLNgk----------
----------gLLQSDQALFTDp--RTRPIVQSYAndqAAFFEDFAKAMVKMGN----------
----

>gi|13399943|pdb|1FHF|A Chain A,
----------qltptfyretcpnLFPIVFGVIFDAsft--------dprIGASLMRFHD
CFVq----------GC-DGSVLLnntdtieseqDALPNinsirGLDVVNDIKTAVensc-pdtVSCADILAIAAEIASV
LGg-gPGWPVPLGRRDSltanrt----------lanqnlPAPFFn---------LTQLKASFAVQGl-NTLDLV
TLSGGHTfGRARCstfinrlynfsntgnpdptlntty-----levlrarcpqnatgdnltnldlstPDQFDNRYYSNLLQln----------
----------gLLQSDQELFSTpgaDTIPIVNSF]SsnqNTFFSNFRVSMIKMGNigvltgdegeirlqcnfvng----------
----

--

>gi|13096480|pdb|1C8I|A Chain A,
----------qgpgggggsvtcpggqstsnsqccVWFDVLDDLQTNfyqgs-----kcesPVRK
ILRIVFHDAIGfspaltaagqfgggGA-DGSIIAhsn----ielAFPANggltdTIEALRAVGINHg-------VSFGDLFAT
AVGMSNCpgsPRLEFLTGRSNSsqpsp----------psliPGPGNt---------VTAILDRMGDAGf-
SPDEVVDLLAAHSlASQEGlnsaifr----------spldstPQVFDTQFYIETLLKgttqpgpslgf----------
aeelspfpgefRMRSDALLARDs—RTACRWQSMTssnEVMGQRYRAAMAKMSVlgfdRnaltdcsd
Vipsavsnnaapvipggltvddievscpsepfpeiatasgplpslapap----------

>gi|2288998 putative peroxidase [Arabidopsis thaliana]
----------mvvggvslfpetaeaivmgpsmqkltwhyykvyntcenAENFVRHQVEIFykn--------dksIA
PKLLRLLYSDCFVs----------GC-DASVLLegpn---sekMAPQNrg-lgGFVLIDKIKIVLeqrc-pgvVSCADI
LNLATRDAVHLAg-aPSYPVFTGRRDGltsdk----------qtvdlPSPSIs---------WDQAMSYFK
NVLDMATLLGSHSmGRTHCsyvvdrlynynktgkpsptmnkyflsemakqcpprtrkgqtdplvylnpdsgsNHSFTSSFYSRILSnk--
----------sVLEVDQQLLYNd—DTKQISKEFFRKSFALSMSKMGAinvlTkIrk
Dcrhin----------

>gi|1403138 A.thaliana mRNA for peroxidase ATP2a, clone EST 163i22t7, and translated products
----------manakpfcllgffclllqlfsifhigngelemnyykescpkAEEIIRQQVETLyyk--------hgnTAVS
WLRNLFHDCVVk----------SC-DASLLLetargveseqKSKRSfg-mrNFKYVKIIKDALekec-stVSCADIA
LSARDGIVMLkgpKIEMIKTGRRDSrgsylg----------dvetliPNHNDs---------LSSVISTFNSIG
i-DVEATVALLGAHSvGRVHCvnlvhrlyptidptldpsyalyl-------kkrcpsptpdpnavlysrndretPMVVDNMYYKN
IMAhk----------gLLVIDDELATDp--RTAPFVAKMAadnNYFHEQFSRGVRLLSEtnp
ltgdqgeirkdcryvn----------

>gi|1922874 I.batatas mRNA for anionic peroxidase, and translated products

masfmkqlslvlsfialalagcavyqntqtamkdqlkvtptwldntlkstnllslglgkpsggklgdeacVFSAVKEVVVAAina--------ea
rMGASLIRLFFHDCFVd----------GC-DAGLLLndtatftgeqTAAGNnnsvrGFAVIEQAKQNVktqmpdms
VSCADILSIAARDSFEKFs-gSTYTVTLGRKDArtanft----------gantqlVGPNEn---------LTSQ
LTKFAAKGf-NGTEMVALLGSHTiGFARCpllcistfinparvstln----------cncsgtvnatglvgldptPTTWDQ
RFSDVVNdq----------gLLFSDNELLKGn—TTNAAVRRYRdamGAFLTDFAAAMV
KSNlppspgvaleirdvcsrvnansvdpceesrllaspd----------

>gi|2887338 Chlamydomonas reinhardtii mRNA for ascorbate peroxidase, complete CDS, and translated products
----------mqsarvsrtarhtrpscrpqravavrvsakvnveQLKALKAELYNYins---------rgCNPIS
VRLGWHDSGTydknia--epargGA-NGSIRFkp------eiDHGANkglaiALAILNPIKKKYp------dVSYADLFQ
MASATAIEASg-gPKIPMRYGRKDAkgpeec----------spdgrlPGAAHpfadg-sgspAEHLRRVF
NDQDIVVLSGGHTlGRARPersgfgaektkytdvgpgtstaspsgatdrpvtpkpvgqqgtswtvnWLEFDNSYFKEIKA
krds----------dllVLPTDACIFEDd—QFRPYAEKYAadqAAFFADYCVSHQKLSElgvewe
egapvtld----------

>gi|1580761 E.coli 0157:H7 katP gene for EHEC-catalase/peroxidase, and translated products
----mikktlpvlillalsgsfstavaadkketqnfyypetldltplrlhspesnpwgadfdyatrfqqlDMEALKKDIKDLlttsqdwwpadyg
hYGPFFIRMAWHGAGTyrty------dgrgGAsGGQQRFep------lnSWPDNvnldkARRLLWPVKKKYgs----sI
SWGDLMVLTGNVALESMg-fKTLGFAGGREDDwesdlvywgpdnkpladnrdkngklqkplaatqmgliyVNPEGP
ggkpdplasAKDIREAFSRMAmdDEETVALIAGGHTfGKAHGaaspekcigagpdgapveeqglgw-----knkcgtgng
kytitsglegawstsPTQFTMQYLKNLYKyewelhkspagayqwkpkkaanivqdahdpsvlhplmMFTTDIALKVDpEY
KKITTRFLndpKAFEQAFARAWFKLTHrdmgpaarylgnevpaesfiwqdplpaadytmidgkdiksLkeqvmdlgipaSeliktawasas
tfrvtdyrggnngarirlqpeinwevnepeklkkvlasltslqrefnkkqsdgkkvsladlivlsgnaaiedaarkagveleipftpgrtdasqeqtdvasfsvleptad
gfrnyysksrshispveslidkasqldltvpemtallgglrvmdintnnsslgvftdtpgvldnkffvnlldmstrwskadkedtyngfdrktgalkwkassvdlifss
npelravaevyasddarnkfihdfvkswnkvmnsdrfdlnnk

>gi|126290 Ligninase III precursor (Lignin peroxidase).
----------mafkqllsavtlalaasaasvtrratcpdgtqlmnaeccALLAVRDDLQNNmfnn------ecgdEAH
EALRLTFHDAIAispameatgqfgggGA-DGSIMIfsd----ietKFHPNiglde VVESFRPFQQRSg-------MGVADF
IQFSGAVGTSNCpgaPTLNAFIGRKDAtqaap----------dglvPEPFHd---------VNTILARFN
DAGdfDELETVWFLIAHSvAAQNDidpavsh----------apfdstPSVMDGQFFIETQL
rgvefigsggie----------gvaespvkgefRLMSDQQIARDn--RTACEWQSFGtdqAKLQNRFQFIFEAMGQlgt
dpttlidcsdvlpvppplstvphfpagitindvepacaetpfptlptdpgpatavaavprd----------
----------=----------

Succinate Dehydrogenase

>lcl|consensus CybS. This family consists of several eukaryotic succinate dehydrogenase [ubiquinone] cytochrome B small subunit, mitochondrial precursor (CybS) proteins. SDHD encodes the small subunit (cybS) of cytochrome b in succinate-ubiquinone oxidoreductase (mitochondrial complex II). Mitochondrial complex II is involved in the Krebs cycle and in the aerobic electron transport chain. It contains four proteins. The catalytic core consists of a flavoprotein and an iron-sulfur protein; these proteins are anchored to the mitochondrial inner membrane by the large subunit of cytochrome b (cybL) and cybS, which together comprise the heme-protein cytochrome b. Mutations in the SDHD gene can lead to hereditary paraganglioma, characterized by the development of benign, vascularised tumours in the head and neck.
----------VRRALLLSAKRSFTLVVAKAAPQPPAGVKGTAND----IVAAPPPASS
KSHGSYHWTVERIVAAALLPLIPAAYF---TP-SPVMDASLAVALTLHCHWGFESCVIDYIRPRVYgD

VLHKAAHYGLYLGSALTLGGLYYFNTNDVGLTKAVKKLWKL----------

>gi|1420658 ORF YOR297c [Saccharomyces cerevisiae]
----------mllfpglkpvlnastvivnpvraVFPGLVLSTKRSFYSINRLNAENKINDIANTSKEasssVQMFKPPE
FSQFKDSYQKDYERIAKYTLIPLTMVPFYasfTGgviNPLLDASLSSIFLIYLQYGFTSCIIDYIPKGKY-
PRWHKLALYCLYGGSMLSLYGIYELETKNNGFVDLVKKLWNEnddhlyifgrn--

>gi|1234843 Highly similar to Sdh4p, Succinate dehydrogenase membrane anchor subunit (Swiss Prot. accession number P37298)
----------msstkflkplcRIRAFHTSIARSFTIPFLPKIPQKPGGVSGTAND----SSYMPPESRAQ
GSYHWIVERGLSLAVLPLIAVPLV---TTgpiSTFTDTFLSLVLLGHCHIGFQSCIIDYISERVYg-KVHH
YAMYLLSLGSFLSFVGIYKLESQEAGLIASLKSLWDNkpvekkrq-----

>gi|585976 SUCCINATE DEHYDROGENASE MEMBRANE ANCHOR SUBUNIT, MITOCHONDRIAL PRECURSOR
----------mmlprsmkfmtgrrifhtaTVRAFQSTAKKSLTIPFLPVLPQKPGGVRGTPND------AYVPPP
ENKLEGSYHWYMEKIFALSVVPLATTAML---TTgplSTAADSFFSVMLLGYCYMEFNSCITDYISER
VYg-VWHKYAMYMLGLGSAVSLFGIYKLETENDGVVGLVKSLWDSsekdnsqkieakk

>gi|6723970 putative succinate dehydrogenase (ubiquinone) reductase complex subunit; TCA cycle; localization mitochondrial; membrane anchor subunit [Schizosaccharomyces pombe]
mannvdtrsantnsptttsfswftnnmlqtrlglgalRQGRLLFAVKSFSTTSVAKIFPPPPQTIKGTVND------AAVFPH
HSKLHGSYHWDFERIIAIAMVPQVMIPLF---TgtsHPLMDAALACTLITHAHLGFESCVIDYFPARRF
K-KLSPLMHWILRGCTVLTLIGVYEFNTNDIGLTEGIKKLWKS----------

>gi|3913479 Succinate dehydrogenase [ubiquinone] cytochrome B small subunit, mitochondrial precursor (CYBS) (Succinate-ubiquinone reductase membrane anchor subunit) (QPS2) (CII-4) (Succinate dehydrogenase complex subunit D)
----------malwrlsvlcgakeGRALFLRTPVVRPALVSAFLQDRPAQGWCGTQH-----IHLSPSHH
SGSKAASLHWTGERVVSVLLLGLIPAAYL---NP---CSAMDYSLAATLTLHSHWGIGQVVTDYVHg----
DAVQKAAKTGLLVLSAFTFAGLCYFNYHDVGICKAVAMLWKL----------

>gi|3913474 Succinate dehydrogenase [ubiquinone] cytochrome B small subunit, mitochondrial precursor (CYBS) (Succinate-ubiquinone reductase membrane anchor subunit)
----------mlsaVRRAIPLSARILRTSLIQRCAGATSAAVTGAAPPqfdpIAAEKGFKPL
HSHGTL-FKIERYFAAAMVPLIPAAYF---IH---GREMDLCLALALTLHVHWGVWGVVNDYGRPFVL
gDTLAAAVRVGAYIFTACLLAGLLYFNEHDVGLTRAFEMVWEL----------

>gi|3913472 Putative succinate dehydrogenase [ubiquinone] cytochrome B small subunit, mitochondrial precursor (CYBS) (Succinate-ubiquinone reductase membrane anchor subunit)
----------MAASLRHMAHFQKALLVARSAPRISTIVRATST--------LNDGASKVP
DHSMHFKLERLWAVGMLPILPASYF---IH---GPVMDAVLTVALTLHIHWGIHGVVYDYARPYVIgE
AAAKAAHVGVYLITGLLLGALLHFNTNDVGITKAFELVFSL----------

>gi|7301044 CG10219-PA [Drosophila melanogaster]
----------mslslllrgavrcnaanlvksARITPLKSYSTLVANVQRKAVVQPLAVAKIVAPVvreiSVSAPRM
ASAGSSHTLLWTVERIVSAGLLAVIPAAFI---AP---SQVLDALMAISVVIHTHWGVEAMVVDYMRP
VVgNVLPKVAHIALIIISVATLGGLFYFIQNDVGLANGIKRFWAIkgkdaeka-----

Thymidylate Kinase

>lcl|consensus Thymidylate kinase.
----------IEGLDGAGKTTQAELLKERLKAQGIK-VVL
TREPGGTPIGELIRELLL--KEEELSPLT---EALLFAADRIEHLEq—KIKPALKQGKTVICDRYLFSGLA
YQGA---AGGVGLDLVWSLNPDVPLP---KPDLTFLLDVDPEVALERIRRRGE----RD-EEEEEQLDFLR

KVRERYLELAR-D-DGRILIIDASNSIEEVHEEI----------

>gi|20149891|pdb|1GSI|A Chain A, Chain A, Crystal Structure Of Mycobacterium Tuberculosis Thymidylate Kinase Complexed With Thymidine Monophosphate (Tmp)
----------mliaIEGVDGAGKRTLVEKLSGAFRAAGRSvAT
LAFPRYGQSVAADIAAEALh-GEHGDLASSvyaMATLFALDRAGAVH----TIQGLCRGYDVVILDRY
VASNAAYSAArlhENAAGKAAAWVQRIEFARLglpKPDWQVLLAVSAELAGERSRGRAQrdpgRArDNYERD
AELQQRTGAVYAELAAqGwGGRWLVVGADVDPGRLAATLappdvps----------
--

>gi|586867 Thymidylate kinase (dTMP kinase)

----msglfitFEGPEGAGKTTVLQEIKNILTAEGLQ-VMATREPGGIDIAEQIREVILneNNILMDPKT---EA
LLYAAARRQHLVe---KVKPALEQGFIVLCDRFIDSPLAYQGY---ARGLGIDEVLSINEFAIGDm—MP
HVTVYFSIDPEEGLKRIYANGSr--eKN-RLDLEKLDFHTKVQEGYQELMKrF-PERFHSVDAGQSKD
LVVQDVlkvidealkkiql----------

>gi|8134529 Thymidylate kinase (dTMP kinase)
----------mfivIEGGEGSGKSSLAKALGDQLVAQDRKVL
LTREPGGCLIGERLRDLILepPHLELSRCC---ELFLFLGSRAQHIQe—VIIPALRDGYIVICERFHDSTIV
YQGI---AEGLGADFVADLCSKVVGPtpfLPNFVLLLDIPADIGLQRKHRQKV----FD-KFEKKPLSYHN
RIREGFLSLASaD-PSRYLVLDARESLASLIDKVmlhtqlglct----------

>gi|2688733 thymidylate kinase (tmk) [Borrelia burgdorferi B31]
-mekiiktkikngkinninvlllknnkfihsidnyyyiiiidnliidtkrkeekifvikilknfycIEGIDGSGKTSITNKLKALCNDESR--
YYFTKEPSSGIIGEMIRKQLMn-FENPLEEST-FAYLYAADRHDHLYkkggILEILNTKSRKIITDRYLF
SSIAYQG----------KLGYELNKNFP-----LPEKVFFIETDPNIAYERIQKNRT----QSdLFELEKYKTFEQIA
LKYLKIFKkL-EKKINVIYINNSIKDNLDKNakkifnlikf----------

>gi|1170718 Thymidylate kinase (dTMP kinase)

----mrgilitIEGINGVGKSTQAMRLKKALECMDYNaVCIRFPNPDTTTGGLILQVLN--KMTEMSSEQ---
LHKLFTKHHSEFSA----EIAALLKLNFIVIVDHYIWSGLAYAQA---------DGITIETKNIF-----KPDYTFF
LSSKKPLNEKPLTLQRLf------ETKEKQETIFTNFTIIMNDVP----KNRLCIIPATLNKEIIHTMIltKtikvfD
nnsclnyikmyddkylnvqdlnlfdfdwqkciednndkeeyddddgfii

>gi|462468 Thymidylate kinase (dTMP kinase)

---msrgalivFEGLDKSGKTTQCMNIMESIPTNTIK--YLNFPQRSTVTGKMIDDYLT--RKKTYNDHI--
VNLLFCANR-WEFAs---FIQEQLEQGITLIVDRYAFSGVAYATA---KG---ASMTLSKSYESGLP---K
PDLVIFLE-SGSKEINRNVGEEI-----Y-EDVAFQQKVLQEYKK-MIEEGE---DIHWQIISSEFEED-VKK
ELiknivieaihtvtgpvgqlwm----------

>gi|2622201 conserved protein [Methanothermobacter thermautotrophicus str. Delta H]
----------mIDGLDGAGKDTHAELIRRRYLERGEhVFR
SHPEDDNPYGKRAREALL--RGGKVNHIR---AAIFYALDVIRSLWlYHWRSNPGPDTLIFSRYLMGV
AYLPGP---LSSVLYRLLSRVLPT-------TEYMFFLDV-SPEESLRRLMERDE-------HEMFENLDDLTST
REKALRLA----DGWYIIN-TEDPIEDVQSRIdeildrldgdvyednvpc----------

>gi|2649268 thymidylate kinase, putative [Archaeoglobus fulgidus DSM 4304]
----------mrclllggftllsrlcrstaassgsfrngcggcnsqgagqperfnfnrntilldgmrfivIDGMDGAGKDTHAEFVRRRYA
ERGs-vIVRTHPSD-SLFGRVAKASLL--RRGKFFHLM---AAIFYFFDVIYSLLr---YYGR----AETVIFVR
YLGGVLYLPER---YARVLYRFFRSVLPT-------SPYMFYLEA-EPEVCMERVARRSE-------SEMFENIE
DFRRVRERAFRIL----KGWKFIN-TNRPIEETRREIerilseldrrfp----------

>gi|2978458 TKRP1; L549.9 [Leishmania major]

mttiaalartlhgganvyrsrldclkvlhaveqsspppwwtpdcsnfvrqaealstsasataarknpvivVEGLDGTGKTLVTRTLAEK
LSGVAIS----TPPPQFTEIRNTFRGQEE---AVARAFYS---AANYIAAEGILAASq---SSVVVVDRWWCS
TCAMALANGCLYDSLp--PS---GAAVYRWPEDLP-----APDAGFLLCVDEAVRVARIRRRAPe-----DA
EERRLSSQREMRCVAMEAYR---RTNMLIEVAAPSYRVAVNSIlrllpesgvthcaapftqaeldsiepf----------
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APPENDIX C: PROCESSED mFAST SEQUENCES

Note: The first sequence (marked in bold) of these proteins is the consensus sequence and the rest are the aligned sequence of that protein

Cytochrome Oxidase

LHGILMILGFGFLMGEAILVARWPLTRFLSKPTWFLLHRVLQILALVLGVIGLLAIFISHNESGIANFYSLHSWLGL
AAFVLAGLQPLSGFLRPLPPSSYRSYLNPYHRFVGLAIFILAIVTI

MALAFCLCMAEAILLFSHSLFFFCSRKTRIRLHWAGQTMAILCAVLGLGFIISSKIRSEMSHLVSWHSWIGALTLLA
TGGQALCGLCLLCPRVSRVARLKLYHLTCGLVVYLMATVTVLLGML

YHPTFMIMGMVFLFGEALLVYRVFRNERKKFSKTLHVILHSCVLVFMLMALKAVFDYHNLHKIVNLVSLHSWIGLSV
VILYFAQYIVGFITYFFPIPIRQLVMPFHQMFGIFIFVSITVAMGI

LHAMFMTIAWMTMVPIAVIFARWPTTKPGGLLIWFHIHRGANLIGIALMIAAFVLILIHKDWKTIGWGGKHAIIGII
ALCLAWLQPFISTLRCSPDSRRPIFNYIHRGIAICIAGYHFTGGRH

LHGILLWVSMGFLMPVGILFIRKAHENGIKVKVFFYLHVIFQILAVVLATIGAILSLRTLENSFDNNHQRLGLALYA
AMWLQFLTGVFKPSRGSKRRLRWFLLHWILGTIVSIVGIVNIYTGI

AHAILMIFGWLLFVPSGFLFARFKEQTLFGSAVWFQIHRAANFMGVVCMCTSMLCIFISTQWTWSKYWTEVHTDLGV
ISTVLAVAQPINSLFRCGPTHSQRIIFNWAHRCAYTLALTAIIIAA

THGVVNAISWGFLLPAGAVTARYLRQMQSIGPTWFYIHAAIQLTGFLLGTIGFSIGIVLGHNSPVTYGLHRSLGIAT
FTAAALQTLALLFRPKTTNKFRRYWKSYHHFVGCVVMGVVNVFQGF

LHAWLVTFGFVFLMAEGMMCFYSWLTVRYSRNYKTAFHVVLQILGGGMGVAGCLIQLIRDDWSISVTLHARLGFAAF
VLCLISLLSGLVAFLARTISPLVNKTFHVVLSFAFVIAMMAQFYGY

MHMFMTGTGFHVLIAQAMMSHSNPLTRWLSHRNKSRFHAILQIVGGSMVLLGSLGKFSSKEVHF
NTWHGRVGGAASFFCAASIVGGFVNYFQPVMPPSELRFRHNLFGLVTFSLGMGAIYLGY

QHALYAILGLFLCVGESLLVCHWWLGDFISENRLNLLHMVLGMVGLWLGLVGIFAKSIFKSKIHEPHFNSKHGLCGL
LGFLLIAGAVASGFALVCFTHLALHVIHRLMGLGFVLLSCSQWFAL

Alcohol Dehydrogenase

MIIKPKVRGFICRTAHPVGCEANVKEQIAYVKKAGKIKNGPKRVLVIGASSGYGLAARIAAAFGGGADTIGVSFERP
GTEKKPGTAGWYNNAAFKKFAEEEGLYAKSINGDAFSDETKTKVIELIKEEFGGKVDLVIYSLAAPRRKDPKSGEVY
RSVLKPIGAPVTGRTLDTEKDQIIETTVEPATEEEIADTVKVMGGEDWELWIDALAEAGVLAEGAKTIAFSYIGPEI
THPIYWDGTIGRAKKDLDQTAHALNEKLAALGGGAYVSVLKALVTQASSAIPALPLYLSLLYKVMKEKGTHEGCIEQ
IYRLFSEKLYGQDRPPVDDEGRLRLDAFKELTDYAGFKKEFLNLFGFGVDGVDYSQDV

MHIKPIIQGVVARSAHPYGCEQAVLQQIQYVKQANPIKSGPKRVLILGASSGFGLAARIALTFGGAADTIGVSFERA
PSETQTGSAGYYNNLFFKQHAEQAGRIAVNLEGDVFSVDMREQVIEAIETYFEGEVDLIIYSIASGMRRKPRSEEFW
RSAIKPIGEAVSGATLLLENDTWIETTLQPASEEEIEGTLRVMGGDDWENWIDTLINAESLAEGCKTIAFSYMGPDV

THPIYLDGTLGRAKIDLHQTSHALNLKLANFDGGAYAVVCKALVTKASVFIPGLSPYLLALYQVMKNKGTHEGCIEQ
MQRLFSDKLYGHSRIPLDSERLIRMDNFQQLGDYAGFKREFMQLNGFEFDQIDYSQSV

MRIEPIIQGVVARSAHPFGCEAAIKKQIAFVKNAPQISQGPKRVLILGASSGFGLAARIALTFGGAADTIGVSFERG
PSEKGTGSAGWYNNVFFKREAEKEGRIAINIVGDAFASETRTQVIEAIETYFEGEVDLVIYSLATGMRPISQPGEFW
RSVIKPFGQTVTGASFDLEHDRWIDTTLESATEEEALHTIKVMGGEDWESWIDTLINAESIAQGCQTIAFSYVGPEI
THPIYLDGTLGRAKIDLHQTSHSLNLKLANFDGAAYATVCKALVTKASVFIPALSPYLLALYRVMKDEKCHEGCIEQ
MQRLFATKLYGQDHISVDGERLVRMDNFQVIGDYQGFKNEFLQLNGFGFDEVDYSQDI

MRIEPLIQGVVARSAHPYGCHASIKEQIEYVKKAPKIKSGPKRVLIIGASSGFGLAARIALTFGGAADTIGVSFERG
PSEKGVGSAGWYNNIFFKQEATHAGRTAINIVGDAFSDSVRNEVIEAIETYFEGEVDLVIYSLAAGVRPKPHSDTFW
RSVIKPIGESVTGASILLENDQWVETTLEPATEEEAEATIKVMGGEDWESWIDTLINTESVAQGCKTIAFSYMGPEV
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MIIKPRVRGFICVTAHPTGCEANVKKQIDYVTTEGPIANGPKRVLVIGASTGYGLAARITAAFGCGADTLGVFFERP
GEEGKPGTSGWYNSAAFHKFAAQKGLYAKSINGDAFSDEIKQLTIDAIKQDLGQVDQVIYSLASPRRTHPKTGEVFN
SALKPIGNAVNLRGLDTDKEVIKESVLQPATQSEIDSTVAVMGGEDWQMWIDALLDAGVLAEGAQTTAFTYLGEKIT
HDIYWNGSIGAAKKDLDQKVLAIRESLAAHGGGARVSVLKAVVTQASSAIPMMPLYLSLLFKVMKEKGTHEGCIEQV
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RSVLKPIGVAHTSNAIDTNKDQIIQATVEPATEQEIADTVAVMGGQDWELWINALAQADVLAPQTRTVAFSYIGTEI
TWPIYWHGALGKAKADLDATSRRLDARLQFLGGGANVAVLKSVVTQASAAIPALPLYIAIVFKVMKEKGLHEGTIEQ
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MIVEPKFRGFICTTSHPIGCKKNVENQIEYVKENGKIEGAKRVLVLGASTGYGLASAIVASEACDAEVLGVSFEREA
KGKRTASAGWYNIESLKKFVEGEGKKFISVNGDAFSNEVKSEVIDLIKENMGKVDLVIYSLAAPKRKDPVSGEVYSS
CLKTVGAPFTSKTLDFHTGEIQNITINPATEEEIEGTRKVMGGEDWMLWIEALKEANVLENGVKTIAYSYIGPEVTY
PIYREGTIGRAKNDLEKTAGEITKVLKSLNGEGYISVNKALVTQASSAIPIVSLYISILYKVMKEKGTHEGCIEQIY
RMFKELYEGNLNLDSENRIRIDDLEENVFELSDAEDFKKEFFKLFGFGLEGVDYSEDV

MIVKAKVKGFIRDVHPYGCRREVLNQIDYCKKAIGFRGPKKVLIVGASSGFGLATRISVAFGGPAHTIGVSYETGAT
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RVVKPTGRGYLLLDAHPVGCFRSVELMRAEVPVPEKPPARRPTALVIGSSSGYGLASTIAGLVRYGIDGVGIGLERP
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VLKPLGAPHTTRNLEFADDQVREVTVAPATEAEAAATVGVMGGEDWSRWITALAERGLLRSGFRTVALTYIGSPLTS
AIYRGGTIGAAKAHLESTARALTERLAAVDGRAFTSVNGALVTQALTAIPGIPLYVSLLRGVLGDRFPSPVAQSLDL
WHQLTRPDVDDSGRIRLDRWELSEPETVTALADTAWFRAQCRALYGFDVPGVDYTVPV

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EFADDQVREVTVAPATEAEAAATVGVMGGEDWSRWITALAERGLLRSGFRTVALTYIGSPLTSAIYRGGTIGAAKAH
LESTARALTERLAAVDGRAFTSVNGALVTQALTAIPGIPLYVSLLRGVLGDRFPSPVAQSLDLWHQLTRPDVDDSGR
IRLDRWELSEPVQAAVAERWRSITPETVTALADTAWFRAQCRALYGFDVPGVDYTVPV

Glukokinase

MKAMGYPRLVGDSGGTNARVALVEIAPAEPLQAETYACADYPSLEEAVQDYLSEHTAVAPRSACFAIAGPIDGDEVR
LTNHDWVFSIARMRAELGLDHLSLINDFAAQALAIPRLGAEDLEQIGGGKPEPNAPRAVLGPGTGLGVAGLVPNGGG
WIPLPGEGGHVDFAPRSEREFQILEYLRARFGRVSAERVLSGPGLVNLYRALCAADGRLPEDLTPAAITERALAGGD
ALARETLSLFCAILGRVAGDLALTLGARGGVYIAGGIVPRILEAADIPVYVILHPQPGLLGAAAALRQP

MGAMGVNFLAGDIGGTKTILALVTINESSPGLAQTYSSPAFPDLVPMVQQFRQEAVLGNPISACFAIAGPVIDNTCR
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YRVFASEGAHGDFAPRSPLEWQLLEYLKKKLGRISIERVVSGMGIAMIYEFLRHQYNREKDQETKAAVSQAALEGTD
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WVPVPGEGGHIDIGPRTERDYQIFPHIERIEGRVTGEQILSGRGLRNLYLGICAADKITPTLETPVDITSAGLDGSN
PQAAETLDLFATYLGRLAGDLALIFMAHGGVYLSGGIPVRILSARDIPVRVITYQLAALTGLSAFARTP

GNHSGGLGLVGDIGGTNARFALVEFDGQDPRLITAYRGEDYGTAEDAIEEYLRKVVKHPDQAVVAVAGPIDHGQVHM
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SLATVNRFCAILGSTAGDIALTLGARGGVFIAGGIAPRIIDILERSIPTHVILHPHTALIGAAVALTPE

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PGEPREVPVFEALQARHGRVSAEHFLSQQGLADIYAALGGGLDDSDEVILARVRDGDETAREALSIFSALLGAFAGD
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KTETYPRLLADIGGTNARFGLEVAPRQIECIEVLRCEDFESLSDAVRFYLSKCKESLKLHGSFAVATPIMGDFVQMT
NNHWTFSIETTRQCLTLKKLLVINDFVAQAYAISAMQENDLAQIGGIKCEINAPKAILGPGTGLGVSTLIQNSDGLK
VLPGEGGHVSFAPFDDLEILVWQYARSKFNHVSAERFLSGSGLVLIYEALSKRKKLSKAELTPQIISECALNGDYPI
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RDAPNIPSFVADVGGTHVRVSVVAAAPASPPQLRTYRCADYPSLSTILNDFLGTRSAVRDCVIASAGFQRSDTVITT
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SSQTLEVFCDFLGSIVGDLVMMYGAQGGVYLAGGILPQLREPLLQHVPVRLIEHGQLGIVGAARWYLNK

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GHADFAPRNELEFQLLKYLLDKIQRVSVERVVSGQGIVAIYQFLRDRKEQQAGQAEKAAIGKAAVQGSDRLSEQALQ
LFIDAYGAEAGNLALKLLPYGGLYIAGGIAPKILPLIENSNFLLSAIPVHIILNQQVGLIGAALCAARL

Glycerol Kinase

***MLADKYILAIDQGTTSSRAIVFDEDGNIVAIAQREFTQIYPQPGWVEHDPLEIWASVRSVLKEALAKAGIKPGEIAA
IGITNQRETTVVWDKETGKPIYNAIVWQDRRTADICEELKADGYEERIREKTGLVLDPYFSATKIKWILDNVPGARE
RAEKGELLFGTIDTWLIWKLTGKVHVTDYSNASRTMLFNIHSLEWDDELLELLGIPRSMLPEVRPSSEIYGVTGIGF
LGAEVPITGVAGDQQAALFGQGCFEPGMAKNTYGTGCFLLMNTGEKPVRSENGLLTTIAWGLDGKVTYALEGSIFVA
GAAVQWLRDGLGLIDDASDSEELAESVEDNGGVYFVPAFTGLGAPYWDSDARGAIFGLTRGTTKAHIARATLESIAY
QTRDVLEAMEKDSGIKLTRLRVDGGASRNNGFWKDLDELAELWPLDKEFEPGMDEEEREELYAGWKKAVKRSLGWRK
D***

LRSVPLIASIDVGTTSSRCILFNRWGQDVSKHQIEYEELFPKPGWVECHPVNVVQCLASSLLSLQTINGLPPYKVIC
MGIANMRETTILWSRRTGKPIVNGIVWNDTRTIKIVRDKWQNDRQLQLRQKTGLPLSTYFSCSKLRWFLDNEPLCTK
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VKRNLPIQGCLGDQSASMVGQLAYKPGAAKCTYGTGCFLLYNTGTKKLISQHGALTTLAFWFPHKPHFALEGSVAVA
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QARAILKAMSSDAFGKLSVLAVDGGMSRSNKLWKDLHDVKNGMEKNEQISPEAHDAERRKHWKYWEVAVERSKGWLK
D

MIGVIDAGTTTIKLAVYDEDKLVAIKKEPVVKHNPKPGWVEIDAEDLARKCVSFADTAIDEYGVEVIAITNQRTTAV
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LGCWEEGDIKATNGTGTFVDLNVGEEPQASPGGLLPLIAWKLKSEMRYMMEGMLFYSGSAVEKLKEIGIYDDVSKTS
EMAFRSKNDDMLLIPSFTGLATPHYVSVPGLLYGISNAMTREDIVKALLESIAFRIAEIVEIMRKEFPYTDRIRCDG
EMSSNDFFLQRIADVTGLKVERGAVLSGTSHLVAGRALGKWKKDFCMPFDKVFEPSLDLSEKYRRWKRLLEISKKLK
V

MRAILSIDQGTTNSKAILVSESGELLARGSSPVGIYPQPGWVEQDPNRIWASVREAISACLAAAVSVEAIAISNQRE
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FGHGAFNPGDGKVTFGTGSSVMTTLPHFIAPERGITTTVAWRLGGKPTFAFEGNILVSAASLPWMTDILGLPDVAAL
VELAATAEPEGPGFVPAFVGLGAPYWDTNARALFSQINFSTTRAQMARAVTDSIAFQVHDVFAAMRAQSPSFGRLFV
DGGPSQNRFLMQCVADMLEHPVIQRDAPEALALGVWSDLNAIAALNSNGNTIATTGESRQRLGIWRDAIARSTLPVT
S

MLADSLLCSVDVGTSGIRLSLYGEDLGLVARYTEELTLYYSGNRVEQDALILAANVRDMLGKAARSGCNVVGLSIYR
GSVVAWRNGKPLSDVITWMDSRGLEEYSKLPLGARLVSKSPVLGKALKPGSPALVMRRLWLNHPGARIWSIDGFLSD
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GCVKATLGTGLFLDAPVEGKPPLFTGDLIPVVNLALPGRVYYGLEGFAAGVGMVFDAFARVLGGFSVLEEKALEPAD
PAPVVPVLAGLRTPYRPLLRGAVLGVSPGFTAASLAKGLIIGTLLTVLSIYRELARRMGGFGELRIGGGLSRLGLLA
SSIASAVGVKVYRSVDYNDSARGAALVAGYASDLLNPPVSLVEVEPLEELSLSGVDDALASEDFSRRLEEIRRSSFR
R

MRIAALDQGTTSTRVLVASQDGSADIQLALRHQQHHPQSGWVEHDPLELLANLQRCLEASGRVDAIGLANQGESCMA
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DAWFLDRLCTFATDVTTASRTALMNLAEGRWDPDLCALFGVPIECLPEIRDTVGHFGVIGNTPLTASVVDQQASLYG
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GFDRPPAIERGLAFVPALSGLACPHWDRSAGAMWLGMDAGTRREDLCQALLEGVVLRSAEVIQAMDGYLKVTDRLSI
DGGLARSPYFAQFLADSLQRRIVTQRFDELTLAARGLGHELAEPRNTRTEFQPRVDAGTARRWQVRFSEAVARTRGW
R

MYVLAIDQSTSGTKAIIFDEKGGIVHRVTVYHKQYYPKPGWVEHDPEEIFRNTLDACRKVIEESGIKPLEIEALAIT
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KLGIISDPSETEKIALSLENNGGVYLVPAFVGLGAPYWRSDVKAAILGLQRNHGKEHVVRAALESIAYQVRDIFEEM
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E

RPIDDIFLALDAGTTDVKAGAYDRSMNLIASCKRRIVYYGQGGVVEQDPHEILEAAKYCLNSILRRIKRYGEPKAIG
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LSVAGDQQASLFGNGCLYPGQAKASYGTGAFILENTGVRVKSDRLLETLFYTYKGKRTYALEGTILSSGSSIDWLVS
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G

MDANGRIVSFAYRLNRQYFPAPGWVEQDPVNLWRNVRITLKKAIEESRIDLTGIASAGVTNQRETVLVWDRKTGRPL
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TVTDHSNASRTMLYDIAKLRWNPDLLDIFGGISELPEVMSSGSAEYGYISKIFDGREVPITADIGDQQSALFGQGCF
NPGDVKATYGTGTFILSNAGTEVPQTSGTLLRTIFYSISGELSYALEGSILASGSVLRWLQNSLHLFRSAKDIEDAA
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N

TPIILAIDEGTTNAKAIAVDRAGRVLAKASVPLQLHPQPGWAEQDPLAIWLAVSQAVEGCLNQLAQVAGIAISNQRE
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DLSRLTDMAESQSGNQGVYFVPALSGLGAPYWDSQARGLFCGLTDATTPAVLARAALESVAYQIADVFFAMENAAHH
LERLRVDGGATSNRWLMQFQADLLQRTLIRNHTAEQDSQQLAALPREVEYIEPRISAEMQDNYSLWQTAIARARFQP
K

Ascorbate Peroxidase

***AAPVVDARYLKDLEKARRELALLIAEKGCAPILVRLAWHDAGTYDKTTKTGGPNGSIRFKLNHGANAGLQIAVKLLE
PIKKKFPWVSYADLFQLAGVTAVEVTGGPKIPFRPGRVDTPEDEGRLPDADKGAGHLRRVFYRMGLSDRDIVALSGA
HTLGRAHKERSGFEGPWTPLKFDNSYFVELLNGESGLLKLPTDKALLQDVFRPLVEKYADEDAFFADYAEAHKKLSE
LGFTFP***

SYPTVSPDYQKAIEKAKRKLRGFIAEKKCAPLILRLAWHSAGTFDSKTKTGGPFGTIKHQLAHGANNGLDIAVRLLE
PIKEQFPIVSYADFYQLAGVVAVEITGGPEVPFHPGREDKPEPEGRLPDATKGSDHLRDVFGAMGLSDQDIVALSGG
HTIGAAHKERSGFEGPWTPLIFDNSYFTELLTGEDGLLQLPSDKALLTDVFRPLVEKYADEDVFFADYAEAHLKLSE
LGFAEA

NYPTVSEDYKKAVEKCRRKLRGLIAEKNCAPIMVRLAWHSAGTFDCQSRTGGPFGTMRFDQAHGANSGIHIALRLLD
PIREQFPTISFADFHQLAGVVAVEVTGGPDIPFHPGREDKPQPEGRLPDATKGCDHLRDVFAQMGLSDKDIVALSGA
HTLGRCHKDRSGFEGAWTPLIFDNSYFKELLSGEEGLLQLVSDKALLDDVFRPLVEKYADEDAFFADYAEAHMKLSE
LGFADA

SHPKCLASDPEQLKSAREDIKELLKTTFCHPILVRLGWHDAGTYNKNIQRGGANGSLRFDLGHGANAGLVNALKLIE
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LGAKFD

AVRVSAKVNVEQLKALKAELYNYINSRGCNPISVRLGWHDSGTYDKNIARGGANGSIRFKIDHGANKGLAIALAILN
PIKKKYPDVSYADLFQMASATAIEASGGPKIPMRYGRKDAKGPDGRLPGAAHPAEHLRRVFYRMGLNDQDIVVLSGG
HTLGRARPERSGFGAEKTWLEFDNSYFKEIKAKRSDLLVLPTDACIFEDQFRPYAEKYADQAAFFADYCVSHQKLSE
LGVEWE

CGPVVDQRYLKDLEGARRDLASIIQRKNAAPVLLRLAFHDAANYNVTNNTGGVNGSVRLRLSQPPNKGIEDGVKFCE
EVKKKHPRVTYADIIQLAGVLAVELSGGPCIDFVPGRMDTNVDKLNIPNPRGGADHLRRTFYQMGLSDKDIVVLSGA
HTLGRARKENSGFNGPFTTLKFDNSYFVELMRGEPGLVKFPTDKALVQDVFRPLVELYAHEGAFFRDYAESHKKLSE
LGFTPS

AAPKVDADYLKHIEGARKELRTIISTKQCAPLMLRLSFHDAGTYDAKTKKGGPNGTVRFELNNPANNGIKTAVDLVE
QVKVKHPKVTYADLYQLAGVVAVEVTGGPVINFVPGRPDVQQDSGSLPLPSGDANHLREVFHRMGLSDRDIVVLSGA
HTLGRANRDRSGVDGPFTPLKFDNSYYVELLKGDPELVKFNTDKVLLQDTFRKYVQLYADEKAFLTHYAESHKKMSE
LGKPKH

VASVEKGRSYEDFQKVYNAIALKLREIGYGPVLVRLAWHISGTWDKHDNTGGSGGTYRFKFNDPSNAGLQNGFKFLE
PIHKEFPWISSGDLFSLGGVTAVQEMQGPKIPWRCGRVDTPEDNGRLPDADKDAGYVRTFFQRLNMNDREVVALMGA
HALGKTHLKNSGYEGPYGNNVFTNEFYLNLLNEDSGYMMLPTDYSLIQDKYLSIVKEYADQDKFFKDFSKAFEKLLE
DGITFP

VASVEKGRSYEDFQKVYNAIALKLREIGYGPVLVRLAWHISGTWDKHDNTGGSGGTYRFKFNDPSNAGLQNGFKFLE
PIHKEFPWISSGDLFSLGGVTAVQEMQGPKIPWRCGRVDTPEDNGRLPDADKDAGYVRTFFQRLNMNDREVVALMGA
HALGKTHLKNSGYEGGGANNVFTNEFYLNLLNEDSGYMMLPTDYSLIQDKYLSIVKEYADQDKFFKDFSKAFEKLLE
NGITFP

AVAPMAKASAATLAECQAECAALVKKASCAPILVRLAWHDSGNYDATTKTGGANGSIRFDMKHGGNAGLPLAVKLLE
PIKKKFPDVGYADLFQMASATAIEVSGGPKIDMKYGRVDAADPEGRLPSAGAPQGHLRRVFGRMGLSDQDIVALSGA
HTLGRAFKNRSGAAPLESWLKFDNRYFTMLLEAEPELLQLATDNALLTDAFRPLVEKYADNAAFCADYAAAHKRLSE
LGSTFE

Glyceraldehyde-3-phosphate Dehydrogenase

***TTNCLAPLAKVLNDNFGIEKGLMTTVHAYTADQKLVDGPHHKDLRRGRAAAPNIIPTSTGAAKAVGLVLPELNGKLT
GMAFRVPTPNVSVVDLTVELEKPGALKGILGYTEDPLVSSDFIGDPHSSIFDAKATIVLNDNFVKLVAWY***

TTNCLAPIVHVLTENFGIETGLMTTIHSYTATQKTVDGVSLKDWRGGRAAAVNIIPSTTGAAKAVGMVIPSTKGKLT
GMSFRVPTPDVSVVDLTFRATRDTYMKGILGFTDEELVSADFINDNRSSVYDSKATLQNNKRFFKVVSWY
NTTALLRTICTVNKVSKVEKVRATIVRRAADQKEVKKGPINSPDPATVPSHHAKDVNSVIRNLDIATMAVIAPTTLM
HMHFINITLKDKVEKKDILSVLESSKYDAEATAELVEVARDLKRDRNPEVMIFSDSIYVKDDEVMLMYAV

NTTGLCRTLKPIDDLCGIKKVRAVMVRRGADPVQVKKGPINAPNPPTVPSHHGPDLKTVMKGVNIHTVALLVPTTLM
HQHNIMVELEDPVEADEIKARLDRASEGLASTAEIMEYAKELGRSRNFEIPVWEESINVVDGELFYMQAV

NTTGLVRTLNAIKDYVDYVYAVMIRRAADPNDIKRGPINAPSVTIPSHHGPDVQTVIPINIETSAFVVPTTIMHVHS
IMVELKKPLTREDVIDIFENTTREKEKGFESTAQLIEFARDLHREWNYEIAVWKESINVKGNRLFYIQAV

NTTGLTRLIYMLKTNFSIGRIRATMLRRVVDPKEDKKGLVNGPDPVAIPSHHGPDVKTVLPDVDIVTTAFKLPTTLM
HVHSLCVEMREAVKAEDVVSALSSAEDGFTSTAKVIEFARELRLRYDYENIVWRESIGVDGNDLFVTQAV

TTNAIVPPLKAMADEFGVESGHVETVHSFTNDQNLLDNYHKSDRRGRSAPLNMVLTETGAASAVAKALPDLGAKISG
SSIRVPVPDVSIAILNLRLSRGTLPLRRQIDFTTSADAVSSDFVGSRHASIVDAGATKVDGDNAILYLWY

TTNAIAPICAILDKAFKIKEGMLTTIHSYTSDQKLIDLAHPLDKRRSRAAASNIIPTTTKAALALHKVLPNLKNKMH
GHSVRVPSLDVSMIDLSLFLEKKKGVLKGVLEIDLKERVSSDFISNPHSVIIAPDLTFTLENMVKIMGWY

TTNCLAPLAKVIHENFGIKQALMSTIHAVTATQPVTDSVMKRDWRSGRACLSNIIPASTGAASALTLVIPELAGRIT
GTSWRVPVQDVSVVDLVVETEKDDELCGIMAYRDDFCVSSDFLTTTTISNFDSKSGIELHSRFFKLVSWY

TTNSLAPMANALNKEFGIQVGTMTTIHAYTATQKVLDGPDRNNFRNARAAAENIIPHSTGAAKAIGLVLPELNGKLD
GHAQRVPVKDGSETELVTILDKKKYESPSFAYNADQIVSTDVLGMTAGSIFDPTQTQVITKQLVKTVAWY

Lactate Dehydrogenase

***MRISAEELKSLIKRVLTQAGVPEEDAKIVADVLVDADLRGVHSHGIGRFPRYVQRLSQGGINPNAQPKIVEEGPATA
QLDGDRAFGQVVAKKAMDLAIEKAKQHGVGVVALRNSNHWGRAGYYVQQAAEAGMIGISMTNSDPMVAPFGGREPIL***

GTNPLAIAFPGKDKPFLLDMATSAIAFGKLLVARRKGKSIPEGWAVDKEGNPTTDPAVVEKGRRLLPFGGHKGYGLS IMIDILSGLLSGGAFGTQVTGTYNEGCNLGQLFIAINPEFFIDGEEFRAKLDAFMDEVKSSEPADEFERVLLPGEIE TLNGIPIDDSVWEKLKSI

IRVPKDRLFSFIVRVLTKLGVPEEDAKIVADNLVMADLRGVESHGVQRLKRYVDGIISGGVNLHPKIRVIREGPSYA
LIDGDEGLGQVVGYRSMKLAIKKAKDTGIGIVIARNSNHYGIAGYYALMAAEEGMIGISMTNSRPLVAPTGGIERIL
GTNPIALAAPTKDKPFLLDMATSVVPIGKLEVYRRKGKDIPEGWAINREGNITTKVEEVFNGGALLPLGGHKGYGLS
LMVDILSGILSGGTWSKYVKNTSEKGSNVCHFFMVIDIEHFIPLEEFKEKISQMIEEIKSSRKHPEFERIWIHGEKG
FLLGIPIYRKVLEELNEI

MRISPEEEVKIIKEILTAMNVPEESSDIVADVTLDADLKGFSSHGIGRFPQYVDGLRHGTIRADGDITIERETESTA
LINGNHIFGHVVAYRAMELAIEKARNTGVGLVGVHDSNHFGVAGYYSDMAVMNDMIGVVIANTEPAVAPIGGRKPIL
GTNPVAIGIPSNRYYVSVDMATSASARGKLLEAARKGESIPENVALDAEGKPTTDPEMALKGSILPFGGHKGYALSF
MIEILAGPLVGAAFGTAVTGTANEMCTKGDLMMAIDPSKMVDPDEFRAQVDEFIEEVKSSGDVLIPGDIESMNIKRR
RAEGIELDEKLLERILGI

MILKPENEKKLIIDVLKKFGVPEEDAKITADVFVDADLKGFTSHGIGRFPQYITALKLGNINPKPDIKIVKESPATA
VIDGDLGLGQVVGKKAMELAIKKAKNVGVGVVATRNANHFGIAGYYSELAMNQDMIGITITNTEPAMAPFGGKEKIL
GTNPIAIAFKGNKYKFSLDMATASIARGKILEALRKKIKIPEGCAVDKDGKPTTDPAKALEGCILPFGGPKGYGLAL
AIEMLSAIGGAEVGTKVKGTANERCTKGDLFIAINPEFFMGKEEFKRKVDELLDEIKNSEPAEGFEILIPGEIEERN
KMDGFEIDKNLYNQLKEI

ITIAAEEAKELVWQKLDGAGLNERDAEKVADVLVHADLRNVHSHGVLHTEHYVNRLLAGGINPGAQPVFKETGPVTG
VLDGDDGFGHVNCDMAMDHAIDMAKKKGVGMVTAVNSSHCGALSYFVQKAADEKLIGMAMTHTDSIVVPFGGRTPIL
GTNPIAYGVPAKHKPFILDMATSKVAFGKILQAREEGKEIPEGWGVDENGEAVTDPDKVVSLSTFGGPKGYGLSIVV
DVFSGLLAGAAFGPHIAKMYNQKRKLGHYVCAINPSFFTDWDTFLEQMDAMIDELQQSPPAVGFERVYVPGEIEQLH
EENGISIARSVYEFLKSR

MKISRETLHQLIENKLCQAGLKREHAATVAEVLVYADARGIHSHGAVRVEYYAERISKGGTNREPEFRLEETGPCSA
ILHADNAAGQVAAKMGMEHAIKTAQQNGVAVVGISRMGHSGAISYFVQQAARAGFIGISMCQSDPMVVPFGGAEIYY
GTNPLAFAAPGEGDILTFDMATTVQAWGKVLDARSRNMSIPDTWAVDKNGVPTTDPFAVHALLPAAGPKGYGLMMMI
DVLSGVLLGLPFGRQVSSMYDAGRNLGQLHIVINPNFFSSSELFRQHLSQTMRELNAITPAPGFNQVYYPGQDQDIK
QREGIEIVDDIYQYLISD

HRFDAQTLHSFIQAVFRQMGSEEQEAKLVADHLIAANLAGHDSHGIGMIPSYVRSWSQGHLQINHHAKTVKEAGAAV
TLDGDRAFGQVAAHEAMALGIEKAHQHGIAAVALHNSHHIGRIGYWAEQCAAAGFVSIHFVSVVPMVAPFHGRDSRF
GTNPFCVVFPRKDNPLLLDYATSAIAFGKTRVAWHKGVPVPPGCLIDVNGVPTTNPAVMQESPLLLTFAEHKGYALA
AMCEILGGALSGGKTTHQETLQTSDAILNCMTTIIINPELFGAPDCNAQTEAFAEWVKASPHDDDKPILLPGEWEVN
TRQGIPLDAGSWQAICDA

MRVSYDELKNEFKRVLLDRQLTEELAEECATAFTDTTQAGAYSHGINRFPRFIQQLEQGDIVPNAIPTKVLSLGSIE
QWDAHQAIGNLTAKKMMDRAIELASQHGVGVIALRNANHWMRGGSYGWQAAEKGYIGICWTNALAVMPPWGAKECRI
GTNPLIIAVPTTPITMVDMSCSMYSYGMLEVHRLAGRQTFVDAGFDDEGNLTRDPSIVEKNRRLLPMGFWKGSGLSI
VLDMIATLLSNGESTVAVTEDKNEYCVSQVFIAIEVDRLIDGKSKDEKLNRIMDYVKTAERSDPTQAVRLPGHEFTT
ILNGIPVDERVWAKLKTL

MKVTFEQLKAAFNRVLISRGVDSETADACAEMFARTTESGVYSHGVNRFPRFIQQLENGDIIPDAQPKRITSLGAIE
QWDAQRSIGNLTAKKMMDRAIELAADHGIGLVALRNANHWMRGGSYGWQAAEKGYIGICWTNSIAVMPPWGAKECRI
GTNPLIVAIPSTPITMVDMSMSMFSYGMLEVNRLAGRQLPVDGGFDDEGNLTKEPGVIEKNRRILPMGYWKGSGMSI
VLDMIATLLSDGASVAEVTQDNSEYGISQIFIAIEVDKLIDGPTRDAKLQRIMDYVTSAERADENQAIRLPGHEFTT
LLNGITVDDSVWAKIQAL

Plant Peroxidase

AESIVRSDVQEAIAASLLRLHFHDCFVGCDGSILLNAPPNGFEVIDPIKAALVSCADILALAARDAVVLAPTWEVPL
GRRDSPSPFDVTQLIAKFARKGDVKDLVALSGAHTGRAHCPTVFDNSYYKNLLNLLQSDQALFTDRTRPIVQSYAAA
FFEDFAKAMVKMGN

LFPIVFGVIFDAIGASLMRLHFHDCFVGCDGSVLLDALPNGLDVVNDIKTAVVSCADILAIAAEIASVLGPGWPVPL
GRRDSPAPFFLTQLKASFAVQGNTLDLVTLSGGHTGRARCPDQFDNRYYSNLLQLLQSDQELFSTDTIPIVNSFSNT
FFSNFRVSMIKMGN

DFQKVYNAIALKYGPVLVRLAWHISGTGSGGTYRFNDPSNGFKFLEPIHKEFISSGDLFSLGGVTAVQEMPKIPWRC
GRVDTPDADKAGYVRTFFQRLNNDREVVALMGAHAGKTHLNNVFTNEFYLNLLNMLPTDYSLIQDKYLSIVKEYADK
FFKDFSKAFEKLLE

VWFDVLDDLQTNPVRKILRIVFHDAIGGADGSIIAAFPANTIEALRAVGINHVSFGDLIQFATAVGMSNCPRLEFLT
GRSNSPGPGNVTAILDRMGDAGSPDEVVDLLAAHSASQEGPQVFDTQFYIETLLRMRSDALLARDRTACRWQSMTEV
MGQRYRAAMAKMSV

AENFVRHQVEIFIAPKLLRLLYSDCFVGCDASVLLMAPQNGFVLIDKIKIVLVSCADILNLATRDAVHLAPSYPVFT
GRRDGPSPSIWDQAMSYFKSRGNVLDMATLLGSHSGRTHCNHSFTSSFYSRILSVLEVDQQLLYNDTKQISKEFSED
FRKSFALSMSKMGA

AEEIIRQQVETLTAVSWLRNLFHDCVVSCDASLLLKSKRSNFKYVKIIKDALVSCADIVALSARDGIVMLKIEMIKT
GRRDSPNHNDLSSVISTFNSIGDVEATVALLGAHSGRVHCPMVVDNMYYKNIMALLVIDDELATDRTAPFVAKMANY
FHEQFSRGVRLLSE

VFSAVKEVVVAAMGASLIRLFFHDCFVGCDAGLLLTAAGNGFAVIEQAKQNVVSCADILSIAARDSFEKFSTYTVTL
GRKDAVGPNELTSQLTKFAAKGNGTEMVALLGSHTGFARCPTTWDQRYFSDVVNLLFSDNELLKGTTNAAVRRYRGA
FLTDFAAAMVKMSN

QLKALKAELYNYCNPISVRLGWHDSGTGANGSIRFDHGANALAILNPIKKKYVSYADLFQMASATAIEASPKIPMRY
GRKDAPGAAHAEHLRRVFYRMGNDQDIVVLSGGHTGRARPWLEFDNSYFKEIKAVLPTDACIFEDQFRPYAEKYAAA
FFADYCVSHQKLSE

DMEALKKDIKDLYGPFFIRMAWHGAGTGAGGQQRFSWPDNARRLLWPVKKKYISWGDLMVLTGNVALESMKTLGFAG
GREDDVNPEGAKDIREAFSRMADEETVALIAGGHTGKAHGPTQFTMQYLKNLYKMFTTDIALKVDEYKKITTRFLKA
FEQAFARAWFKLTH

ALLAVRDDLQNNEAHEALRLTFHDAIAGADGSIMIKFHPNVVESFRPFQQRSMGVADFIQFSGAVGTSNCPTLNAFI
GRKDAPEPFHVNTILARFNDAGDELETVWFLIAHSAAQNDPSVMDGQFFIETQLRLMSDQQIARDRTACEWQSFGAK
LQNRFQFIFEAMGQ

Succinate Dehydrogenase

VRRALLLSAKRSFTLVVAKAAPQPPAGVKGTANDIVAAPPPASSKSHGSYHWTVERIVAAALLPLIPAAYFTPSPVM
DASLAVALTLHCHWGFESCVIDYIRPRVYDVLHKAYLGSALTLGGLYYFNTNDVGLTKAVKKLWKL

VFPGLVLSTKRSFYSINRLNAENKINDIANTSKEVQMFKPPEFSQFKDSYQKDYERIAKYTLIPLTMVPFYTGNPLL
DASLSSIFLIYLQYGFTSCIIDYIPKGKYPRWHKLYGGSMLSLYGIYELETKNNGFVDLVKKLWNE

RIRAFHTSIARSFTIPFLPKIPQKPGGVSGTANDSSYMPPESRAQGSYHWIVERGLSLAVLPLIAVPLVTTSTFTDT
FLSLVLLGHCHIGFQSCIIDYISERVYKVHHYAMYSLGSFLSFVGIYKLESQEAGLIASLKSLWDN

TVRAFQSTAKKSLTIPFLPVLPQKPGGVRGTPNDAYVPPPENKLEGSYHWYMEKIFALSVVPLATTAMLTTSTAADS
FFSVMLLGYCYMEFNSCITDYISERVYVWHKYAMYGLGSAVSLFGIYKLETENDGVVGLVKSLWDS

RQGRLLFAVKSFSTTSVAKIFPPPPQTIKGTVNDAAVFPHHSKLHGSYHWDFERIIAIAMVPQVMIPLFTHPLMDAA
LACTLITHAHLGFESCVIDYFPARRFKLSPLMHWIRGCTVLTLIGVYEFNTNDIGLTEGIKKLWKS

GRALFLRTPVVRPALVSAFLQDRPAQGWCGTQHIHLSPSHHSGSKAASLHWTGERVVSVLLLGLIPAAYLNPCSAMD
YSLAATLTLHSHWGIGQVVTDYVHDAVQKAAKTGLLVLSAFTFAGLCYFNYHDVGICKAVAMLWKL

VRRAIPLSARILRTSLIQRCAGATSAAVTGAAPPIAAEKGFKPLHSHGTLFKIERYFAAAMVPLIPAAYFIHGREMD
LCLALALTLHVHWGVWGVVNDYGRPFVLDTLAAASYIFTACLLAGLLYFNEHDVGLTRAFEMVWEL

MAASLRHMAHFQKALLVARSAPRISTIVRATSTLNDGASKVPDHSMHFKLERLWAVGMLPILPASYFIHGPVMDAVL
TVALTLHIHWGIHGVVYDYARPYVIEAAAKAAHVGYLITGLLLGALLHFNTNDVGITKAFELVFSL

ARITPLKSYSTLVANVQRKAVVQPLAVAKIVAPVSVSAPRMASAGSSHTLLWTVERIVSAGLLAVIPAAFIAPSQVL
DALMAISVVIHTHWGVEAMVVDYMRPSVVNVLPKVIIISVATLGGLFYFIQNDVGLANGIKRFWAI

Thymidylate Kinase

***IEGLDGAGKTTQAELLKERLKAQGIKVVLTREPGGTPIGELIRELLLKEEELSPLTEALLFAADRIEHLEKIKPALK
QGKTVICDRYLFSGLAYQGAAGGVGLDLVWSLNPDVPLPKPDLTFLLDVDPEVALDFLRKVRERYLELARDDGRILI
IDASNSIEEVHEEI***

IEGVDGAGKRTLVEKLSGAFRAAGRSATLAFPRYGQSVAADIAAEALGEHGDLASSMATLFALDRAGAVHTIQGLCR
GYDVVILDRYVASNAAYSAAENAAGKAAAWVQRIEFARLKPDWQVLLAVSAELAGELQQRTGAVYAELAAGGGRWLV
VGADVDPGRLAATL

FEGPEGAGKTTVLQEIKNILTAEGLQVMATREPGGIDIAEQIREVILNNILMDPKTEALLYAAARRQHLVKVKPALE
QGFIVLCDRFIDSPLAYQGYARGLGIDEVLSINEFAIGDMPHVTVYFSIDPEEGLDFHTKVQEGYQELMKFPERFHS
VDAGQSKDLVVQDV

IEGGEGSGKSSLAKALGDQLVAQDRKVLLTREPGGCLIGERLRDLILPHLELSRCCELFLFLGSRAQHIQVIIPALR
DGYIVICERFHDSTIVYQGIAEGLGADFVADLCSKVVGPLPNFVLLLDIPADIGLSYHNRIREGFLSLASDPSRYLV
LDARESLASLIDKV

IEGIDGSGKTSITNKLKALCNDESRYYFTKEPSSGIIGEMIRKQLMFENPLEESTFAYLYAADRHDHLYILEILNTK
SRKIITDRYLFSSIAYQGKLGYELNKNFPLPEKVFFIETDPNIAYERIQKNRTQSKTFEQIALKYLKIFKLEKKINV
IYINNSIKDNLDKN

IEGINGVGKSTQAMRLKKALECMDYNVCIRFPNPDTTTGGLILQVLNKMTEMSSEQLHKLFTKHHSEFSAEIAALLK
LNFIVIVDHYIWSGLAYAQADGITIETKNIFKPDYTFFLSSKKPLNEKPLTLQRLQETIFTNFTIIMNDVPKNRLCI
IPATLNKEIIHTMI

FEGLDKSGKTTQCMNIMESIPTNTIKYLNFPQRSTVTGKMIDDYLTRKKTYNDHIVNLLFCANRWEFAFIQEQLEQG
ITLIVDRYAFSGVAYATAKGASMTLSKSYESGLPKPDLVIFLESGSKEINRNVGEFQQKVLQEYKKMIEEGEDIHWQ
IISSEFEEDVKKEL

IDGLDGAGKDTHAELIRRRYLERGEVFRSHPEDDNPYGKRAREALLRGGKVNHIRAAIFYALDVIRSLWYHWRSNPG
PDTLIFSRYLMGVAYLPGPLSSVLYRLLSRVLPTTEYMFFLDVSPEESLRRLMERENLDDLTSTREKALRLADGWYI
INTEDPIEDVQSRI

IDGMDGAGKDTHAEFVRRRYAERGIVRTHPSDSLFGRVAKASLLRRGKFFHLMAAIFYFFDVIYSLLYYGRAETVIF
VRYLGGVLYLPERYARVLYRFFRSVLPTSPYMFYLEAEPEVCMERVARRSESEMFENIEDFRRVRERAFRILKGWKF
INTNRPIEETRREI

VEGLDGTGKTLVTRTLAEKLSGVAISTPPPQFTEIRNTFRGQEEAVARAFYSAANYIAAEGILAASSSVVVVDRWWC
STCAMALANGCLYDSLPSGAAVYRWPEDLPAPDAGFLLCVDEAVRVARIRRRAPDLSSQREMRCVAMEAYRRTNMLI
EVAAPSYRVAVNSI

APPENDIX D: VALIDANTION INPUT SEQUECNES

Cytochrome Oxidase

α

ILGFGFLMGEAILVARWPLTRFTWFRVLQILARSYLNLVLGVIGLLAIFISHNAIVESGIANFYSLLHGILMHSWLG
LAAFVLAGLQPLSGLLHFLSKPLRPLPPSSYPYHRFVGLAIFILTI

β

THGVVSWGFLLPAGAVTARYLRQMQSIGFYIHAAIQLTGFLLGTIGFSIGIHNSPVTYGLHRSLGINAIATFTAAAL
QTLALLFRPKTTNKFPTWRRYWKSYHHFVGCVVMGVVVLGNVFQGF

γ

GWVPSGSAVWGFLFAIFISTQWRIFEQTLFKAHAILMNSLFRCGPTWSKYWTFFQIHLLRCAYTLALTFRAANFMQR
IIFGVVCMCTSMLCEVHTDLGVISTVLAVAQPITHSNWAHAIIIAA

Alcohol Dehydrogenase

α

PKVRRTAHKEQVKKAGKIKNGPKRVLVIGASSGYGLAARIAAAFGIGVSFERPGFIEKKPMIIKGGPVCETAIAEEY
GWYNNAAFKAPRKFAEEEGLKSGYAKSINGKPIGDAFSDETGLDAHALNEGADTKTKTVEVTFGGGGKVDLVIYSLA
REAGVKDKTIAPANVEVYRIYWSVLAPVTGRTTEKDQIIETPATEEEIADTVKVMEDWELWIALAEGAFSYIGPEIT
HPDGTIGRAKKDLDQTKLAALGGGAYVSVLKALVIELIKCGTDDEQASAFSAIPALPLYDALLSLLNLFGFYKVMKE
YSQDVKGTHEGCIEQIYRLFSEKLYGQDRPPVGRLRLDKELTDYAGFKKEFLGVDGVD

β

KTHPLIIIGIVFARLKGEKTKAKNAGNDVTGVILEGGHGAFILHPFGRATLYASEMATVGWGAAAFDAEQKMRDRWE
AKMPTTEIIEDLFWPIPNPQEYGLYSRSIKRSGVVKIGASSGAFELHRSKVALAGAYIAAFLRQVLSAEESGDREKV
RFFLLVGSAKENYRDEIYLGDMVFQRSIHTKVINKKASVYAIPAVNAVSPASKVKLMDVTVAVQVADERLLTLGWRR
TTDYDFKADADRQTRTEGLGALADHVDYEAIDELIIIPIVYNDGSTVPLAVELAKRGQKVKPIAHGKAGCQFETSNA
IADQGYREANDPATETSADTLQFGNLLANGGGFPLTTITRQVSYRLISCTLWQAPDLD

γ

HPKTRTHPLIITLYIGIVFARFFLLRLKGEKTKAAFDAKNAGNDVTTEIIFGVILEGGHVKIGASGAFILFGKVINA
ASEMDWEATVGWAVSPGAAEQKMPTWPIPNPQEGVSGSKVALAGAYIAAFAEEMRAKRSGDREKEDLVVGSAKEIYS
RYGLYSIKRSLGDMVAFELHRFQRSIHKKASVYAIPAVNASKDVTVAVQVLGEAIDELIIIPIVYNDGSTVKVKPIA
HGKATSNAIYREANDPADTLQFGNGVENYRDKLLRQADERLLTVLPLAVELASMGGFPLTGCQFERGQKTIADQGTR
QVSYWATETSRRTRLISNLLACTLWQAPDRQTRTDLDAEGTDYDFLKADVDYDHGALA

Glukokinase

α

YPRLVGDSGGVALVEIAPAEPEAVQDYLSEHTAVAPRSACFAIAMEVRTNARLTNHDWRALQAETYACADYPSLEEL
GLDHLSLINDFAAQALAIPAAITERALAGGPRLGAKAMGGPIDGDEDLEQIGGGKPVFSIEYLRARFGRVSARMEPN
APADIPVYVILHLVNLYRAAAAALRQPLCARAVLGPGTGTLSLFCAILGRLGVAGLVPNGGGWIPLPGEGGHVDFAP
RSEREFQILAERVLSGPGADGRLPEDLTDALAREVAGDLALTLGARGGVYIAGGIVPRILEAPQPGLLG

β

VLDFREHGAFAEQTFSIETCLKKLLVIFVAIMGAISECLVSKGGGQACIYATRMKYGPPESFWLYFTQIERCKCPDE
SFARDAENDVKEIGIGDYRLVSELNSDDLEVAFLPADGMGGAEPGTLLAHPSARSSGLIKTLPIAVAKMLTLSNVHS
LVAPSLSGIKDLSLQAIIGVPKARTGVKAEVVQEQGATRQYENDRKKQYAGLTPRFIQIIIPSIPALEGKTLILLLK
CISIFNDLAVIGVNGLEVYSANGGDYFKLYLRFCDACTTNNHWFGHVLNTLDTFCSKLLGLGGTALTLR

γ

KYGTRQIEVLDFRSKCPDFVKEHGAFAEQTNNHWTFSIETCLTLKLLKKLLVINVARDFVAIMGQACIYAMRCEEIG
IVSELFGHVLMLGLGGSAENDHSLVAPSLSGIKAIIGVPKARTGVKAEVDLSLQNSDDLEVAFLPADGMGGGAISEC

LVSKGGAEPGTLLAHPSAPPESFWLYFTRSSGLIKTLPIALLKCISIFNDLAVIGVNGLEVYSANLRFCDACTVQEQ
GATRQYENDRKKQYAGLTPRFIQIIIPSIPVAKKTLILALEGNGDYRLTLDTFCSTALTLRGGDYFKLY

Glycerol Kinase

α

MLADKYILASIVFDEDGNIVAIAQREFTQIYWVEHDPLEIWASVRSVLAKAGIKPGEIAAIGITQGTTQRETSRATV
VWDKETGKPIYNPQPGAIVWQDRRTADICEELKEALKADGYEERIREKTGLNIDVLDPYFSATHSLEKIKWILDNLG
IPVPGARERAESSEIYGKGELLFGTIDQQATWLIWKLTGKVHAKNVTDYSNASRTMLFNIWDDELLELRSMLPEVRP
VTGIGFLGAEVPITGVAGDALFGQGCFEPGMTYGTGCFLLMNVRSENGLLTLDGKVTYALEGSIFVAGAAVQWLRDI
DDASDSEELAENGGVTGEKPYFVPAFTGTIAWGLGAPYWDSDGGASRARGAIFGLTRGTTKAHGLGLIARATMDEEL
ESIAYQSVEDTRDVLEAMEKRKDSRKDGIKLTRLRVDNNGFWKDLDELAELWPLDKEFEPGEREELYAGWKKAVSLG
W

β

TSRTIDSLEWDSDLLLRPIDDSVVMLEQDPHRPITKLISCLNSILRRIKRYGEPKAIGITNQRESVLAWEPLSESTD
IYFNEVIRSFLSTVIIEKLLEPLHILIAEWKDEILEAAKYMLADIRGYISGLSQADHSNAKENSFNEMALDAGTTGI
FLGAYDRSMNLIAVREALNIKPLPEVKRTSDSYGQAFEIVGISEEILVKLGISKNQGLKSVASYGTGAFILSDRLLE
TLFYTYKGKRIDCKRRIVYPGSVPALSGLGSPFYSYYGQGGGKRGAQLSLDLKEDGGLSKSDRYLAVPILTDVKARK
HIPNVGQVIKDKTGLISDPYPRSILFSATKIKWHVLLVENIKRSIDEVSAGGKEDSNHKNYVITTLDSWLVKNKVKL
GSTTREFGNGCTYALEGTILSSGKGYSSIDWLVRKTSAGDEIAEKFQQASRAEQIERSNLLDMYGKRDNSWRSFLLS
V

γ

TDHSNASRTMLFNIDSLEWDSDLLEIVGISEEILRPIDDIFLALDAGTTDVKAGAYDRSMNLIASCKRRIVYYGQGG
VVEQDPHEILEAAKYCLNSILRRIKRYGEPKAIGITNQRESVLAWEPLYPGSVPALSGLGSPFYSSESTDIYEVIRS
FLEAQAFLSTVIIEEMRKHIKLLEPLHIDGGLSKSDLIAEMLADIRGYISGLSQAKASYGTGAFILENTGVRVKSDR
LLETLFYTYKGKRIDGRPITKLISWKDKRGAQLSLDLKERYGQVIKDKTGLISDPYFSATKIKWLVENIKRSSNHKN
YVITTLDSWLVKNLNIKPLPEVKRTSDSYGKVKLGSTTREFGNGCTYALEGTILSSGSSIDWLVSLAVPILSVAGDQ
QASLGLKSVPRSILRAEQIERSHVLNLLDMKGYYGIDERKTVSAGGKEFNPNDKRDEIAEKFNSWRSFLLSVISKNQ
G

Ascorbate Peroxidase

α

AAPLLIAEKGCAPILVRLAWHDAGTYDKTTKLNHGANAGLQIAVKLRYLKDLEKARRELAPWVSYADLFQLGPKIPF
RHKLEPIKKKFVVDAEDEGRLPDADKGAGLNGESGLLKHLRRVFYRMGLFRPLVEAGVTAVEVTGGPNGSIRFKTGK
YADKLSELGFTFPPGRVDTPSDRDIVALSGAHTLGRAHKERSGFEGPWTPLKFDNSYFVELLPTDKALLQDVEDAFF
ADYAEA

β

YEGARRDLASIIVNGSVVLSQPPNKGIEDGVKDQRTLHPRVDAASGFNGQLNQRPVLLRLAANYNVTGNTGFDNSYL
SGGRARKENPFTTLKAAVEGPCIDFVPFCEVDKPEVKKKAHCGPGKDIVVDLDKLNIANPRHGGADDIIHLRRTFYL
SGQGVLMKALVQDVTYFFRPLVELYAGLSRMRGEPLVRLRDTNKNAKKLSELGFTPSFVELMGLVKFPTDHEGAFFR
DYAESH

γ

CGPDQRYEGARRDLASIIQRPVLLRLAANYNVTGVNGSVVLSQPPNKGIEDGVKFCEVDKPEVKKKAHTLHPRVDAA
SGFNGQLNNTGFDNSYAAVEGPCIDFVPGKDIVVDLDKLNIANPRHGGADDIIHLRRTFYLSGQGVLMGLSRMRGEP
LVRLRDTNKNALSGGRARKENPFTTLKFVELMGLVKFPTDKALVQDVTYFFRPLVELYAHEGAFFRDYAESHKKLSE
LGFTPS

Glyceraldehyde-3-phosphate Dehydrogenase

α

NDLLHKSRAPLVLNVKAFAGRRQIDRFTSKSDASDTTPMADESGDIRVDGVYLTPLPHTVTAISNFVNFKGMRGGTL
PSATLSSRATYGLGVHGAVSAVELRHSALQDNYDRNLWASSIKDAIVVPETGDVAISEAIVAAILLSNPD

β

RVVDPKEDKKGLVNGPDPVAIPSHTTGLTRLIYMLKTNFSIGRIRATMLRSLCVEMREAVKAEDVVSALSSAEDGHG
PDVKTVLYDYENIVWRESIGVDGNDLFVTQAVPDVDIVTTAFKLPTTLMHVHNFTSTAKVIEFARELRLR

γ

TTPMADESGHTVTNDLLHKSRAPLVLNVKAFGAVSAVELRHSALQDNYDRAGRRQIDRFTSKSDASDAISNFVNFKG
MRGGTLPSAGLGVHNLWASSIKDAIVDIRVDGVYLTPLPVPETGDVAISEAIVAAILLSNPDTLSSRATY

Lactate Dehydrogenase

α

SLIKRVLTKIVADVLVDADLRGVHSHIVEEMRISAEELKGPATAQLQAGVPEEDADSNHWGRAGYYGDRAFGQVVAK
KAMDLAIEKAKQHGVGGIGRFPRYVQRLSQGGINPNAQPKVVALRNVQQAAEAGMIGISMEPILGTNPLAIAFPGKD
KPGKLLVARRKGKSIPEGWAVDKEGNGIPIDDSVWEKLKSINSDPMVAPFGGRVEKGRRLLPFGGHKGYGFLLDMAT
SDAFMDEVKSSEPAIAFLSIMIDILSGLLSGGAFGTQVTNPTTDPAVTGTYNEGCNLGQLFIAINPEFFIDGEEFRA
KLADEFERVLLPGEIETL

β

WQKLDGAGLNERDANVHSHGVLHTEHYVNRLLAGAEEAKELVETGPVTGVLDGDDGFGHEKVADVLVHADLRVNCDM
AMDHAIDMAKKVVPFGGRTPILGTNPIAYGVPAKHKPFILDMATSKVAFGKILQAREEGKEIPEAVTDPDKVVSLSI
GYGLSISTFGGPKKGGINPGAQPVFKITIAVGMVTAVNSSHCGALSYEGWGVDENGFVQKAADLGHYVCAINPSFEK
LIGMAMTHTDVVDVFSGLLAGAAFGHEENGISIARSVYEFLKSRPHIAKMYNQKRKFTDWDTFLEQMDAMIDELQQS
PPAVGFERVYVPGEIEQL

γ

HRQTLHSAVFMGSEEQEAADHAAGHHGIPSYWFDQGHQLNRHAKKEKVALIGAHGIAAANHLSHVTHRIGIQIAQGD
NYLGWSLEKAHQCDIALGMGAGDRVHFVRSAFVASVRAFIAMAITQAVAVSISPFHGFGFCVVPQADDLLHATVELS
AIPTAGLAVGFTNPYARAFAMPFGKLGVVSCKPMTRHEVSREIDAWNGVTNPKTFPCVGKGIINGLTTCNATLTLQT
EALWVKADESDDDKPFLFGAPIPAPGEWEVNMLHQGELDIYVRSWAVGDQAICESPLLAEHKLACEIAGGHQTSDAI
MQHLTPNPTIPQNPLDAA

Plant Peroxidase

α

AEASLLRLHFHDCFVGCDFEVIDPIKAALVSCADILALAAWEVPLSIVRSDVQSPFDVTQLIAGSILLNASYEAIAP
PNGKFARKGDVQALFTDRDAVVLAKAMVKMGNPTHTGRAHCPTVFDNGRRDSPYKNLLNLLQSDVQSYRTRPIKDLV
ALSGAAAAFFEDFA

β

IEQQNSCEAIFGRAKKTGDVRYAVVAGTVSHTLLVDALLTNGRVRQCWGLLMGLIDDEKFSAAIEKMLFALYTVSRT
SFFHCAAATGGSAKVVAASRLFCFGNMLDAFLFAMNGTLFEPPTAARVQSNSNEKDGTAATDNDVTDVSVFVKFGVA
KVGAASYFLLLTNR

γ

SAKVVAASRLFCFVDALLTNGIEQQNSCEAILMGLIDDEKFSLYTVGTLFGRAKKTGDVRYAVVAGTVSHTLLAATG
GRVRQCWGLFAVFVKFGVAKVGAAEPPTAARVQSNSNEKDGTAATDNDVTDVSAAIEKMLFSYFLLLTNRSRTSFFH
CAGNMLDAFLFAMN

Succinate Dehydrogenase

α

VRRALLAKAAPQPPAAPPPASSKSHGSYHRPRVYDLHKAYLGSAWTVERIVFTPSPVMDLSAKRSFTLAGVKGTAND
IVHCHWGFESCTKAVKKLWKLVIDYILTLGGTLVVASLAVALLYYFNTNDVGLAAALLPLIPAAYV

β

ALNPAQWPCSGHDSKLASKKASWAKAASWVHTVGGLVYGFLCDYYTLALHKLTVWIGGRPPMPSAVLAHSAVQVNVG
ICVAMLVLADSLLFLQPGRRSACHIHLHALSHTERQVTTDRVSAFHGTQGLLIAYDGLLVLTFAYF

γ

GFLRPPMPSAVLAHSAVQVVLADSLLFLQPALNPAQWPCSGCHIHLHALSHTERQHDSKLASKKASWAKAASWVHTV
GGLVYGRRSAVTTDRVSAFHGTQGLCDYYTLALHKLTVWIGGLIAYDGLLVLTFAYFNVGICVAML

Thymidylate Kinase

α

LLKERLKAQGIKVVLLKEEELSPLTEALLFAADRIELDGAGKTTQAEHEEILDLVWSLNPDGKTVICDRYLFSGLAY
TREPGGTPIGELIRELLQGAAGEVALDFLRKVRERGVGLIIDASNSIEEVHLEKIKPALKQIEGVPLPKPDLTFLLD
VDPYLELARDDGRI

β

MESIPTNTIKYLNFPQTYNDHIVNLLFCANRWEFAFILDKSGKTTQCVDRYAFSGVAYATRSTVTGKMIDDYLTRKK
AKYKKMIEESMTLSKSEGESGLNIQGITLIFLESGSFQQKVGEDIYQEQLEEEDVKKPKPDLVIGKEINRNVGEALQ
EMELFHWQIISSEF

γ

IGSITNKDESFTKGIIGEKQLENPLTFAYGESGADKHALCRYYLEPNTMIRMFTEESDRYRTDPLNLEYYLYIKNLI
LSSEIDFSSINIAKLPTAKSEKYQVRKGLRKLGNIAYEDHQSEQIAIFKLVIFPSIKDKNIIFFIETNRIQKNKTFL
KYLKEKKYINNNLD

APPENDIX E: NORMALIZED TABLE

#	A	R	N	D	C	Q	E
001	-0.26339	-0.14633	1.29747	1.33650	0.90725	-0.18535	-0.49752
002	-0.46916	-0.48126	-1.13506	-0.65077	0.08777	-1.20771	-0.63866
003	0.23995	-0.86926	-0.83530	-1.03904	1.04356	-0.28069	-0.97112
004	0.64078	-0.67883	-0.89282	-1.04737	0.24846	-0.60750	-0.94037
005	1.59222	-0.15667	-0.77607	-0.44815	-1.83270	-0.44815	0.60847
006	0.15267	-0.16540	-1.24687	-0.61071	-0.61071	-0.16540	-1.24687
007	-1.65324	0.55421	1.16478	1.16478	0.55421	-0.38513	-0.90176
008	-0.84129	1.23181	0.43631	1.01486	-0.97388	0.79790	0.84611
009	-1.39328	0.91591	-0.44916	-0.74752	-0.75161	0.12302	-0.08133
010	-0.07600	-0.88802	-0.92579	-0.96356	1.35918	-0.91635	-1.22794
011	0.36272	-0.71629	-0.75482	-0.93787	0.80588	-1.18835	-1.40030
012	0.57033	-0.73022	-0.98078	-0.64669	-1.39839	-0.33647	-1.14783
013	0.17714	0.08728	-0.68291	-0.68291	-2.15912	-0.09242	-1.28623
014	0.73660	0.82250	1.03725	0.73660	0.46816	1.12316	0.62922
015	-0.01311	0.44918	-1.20012	-1.67492	-0.85027	-0.53790	-0.75031
016	0.17106	0.18442	0.43718	0.25709	0.20472	0.25763	0.23465
017	-0.52205	-0.29787	1.41449	1.46219	1.08537	-0.40758	-0.77963
018	0.20927	0.35875	0.58298	0.39612	0.65772	0.02242	0.39612
019	1.33935	-0.53223	-1.10875	-0.31499	-1.05026	0.77119	1.77383
020	-0.58659	0.25627	-1.25860	-0.78022	2.20398	-0.14237	-0.88273
021	-0.63202	0.11427	0.48743	0.48743	-0.16558	0.11427	0.11427
022	-1.32955	1.18096	-0.42781	-0.72497	-0.48929	0.04354	-0.25361
023	-0.65837	-1.05010	-0.44061	0.77838	2.23998	-0.00804	0.60677
024	-0.94255	0.20092	1.21372	0.69098	0.62564	-0.41982	-0.51783
025	-1.05406	0.28812	1.20325	-0.13338	0.06073	-0.98196	-1.75843
026	-1.77951	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
027	-1.22540	0.52517	0.52517	0.52517	-1.22540	0.52517	0.52517
028	-0.86438	0.95537	-0.86438	-0.86438	-0.86438	0.95537	0.95537
029	-1.41305	1.59344	-0.21045	-0.21045	-0.81175	0.39084	0.39084
030	-0.48733	-0.48733	1.94935	1.94935	-0.48733	-0.48733	1.94935
031	-0.97467	0.97467	0.97467	-0.97467	0.97467	0.97467	-0.97467
032	-1.42102	1.18214	-0.39153	-0.64360	-0.80380	0.21861	0.07727
033	-1.26448	1.25303	-0.23458	-0.46345	-0.80675	0.22314	0.45200
034	-0.80918	1.98110	0.82206	0.26400	-1.06674	1.16548	0.22107
035	0.61072	-1.50112	-0.87327	-0.70204	1.01026	-1.15866	-0.53081
036	1.46563	-1.17515	-0.77903	-0.64699	1.72971	-1.04311	-0.77903
037	-0.90324	-0.11307	1.54899	1.27652	0.54085	-0.03133	-0.68526
038	1.49419	-0.07115	-1.17400	0.03557	-1.06728	0.39133	1.81437
039	-0.53898	-0.26745	-0.37606	-1.32641	0.43851	0.19414	-1.78801
040	-0.68526	0.05040	1.27652	1.44000	-0.08582	-0.08582	-0.11307
041	0.49720	-1.00947	-0.35362	1.79118	-0.61951	0.37312	2.53566
042	0.42023	0.52826	-0.89772	-0.85451	0.22578	0.46344	0.50666
043	-0.84020	-2.04767	1.57474	0.09894	-1.00790	-0.67249	0.30019

044	-1.00085	0.53892	1.39435	0.15397	-0.10265	-0.61591	-0.85115
045	-0.37772	-0.29187	-0.80695	-1.40787	-0.35626	1.31773	-1.47226
046	-0.66101	-0.29035	0.47568	-0.41390	0.22857	-0.90812	-1.15522
047	-0.69403	-0.19909	1.98311	0.92575	0.81327	0.25084	-0.13160
048	-0.63179	0.15320	0.35577	0.83690	-1.16356	-0.55582	-0.35324
049	-0.79294	-0.51665	1.99756	1.61076	1.66601	-0.40614	-0.90346
050	-0.13871	0.35375	-0.02380	0.41942	-0.51627	0.22243	-0.40136
051	-0.84744	0.29678	1.94162	1.72707	0.61860	-0.81169	-0.09654
052	-0.88429	-0.07493	0.10491	-0.19484	1.21402	0.31474	-0.70443
053	-0.65777	0.17717	1.21576	1.31759	-0.08756	-0.25048	-0.33194
054	-0.61075	-0.40603	-0.36703	-1.65387	0.59808	-1.13718	-0.95196
055	-0.35823	-0.36799	-0.96341	-0.97317	0.46169	-0.67058	-1.55883
056	0.21789	-0.64003	-1.01050	-1.19573	0.54936	-1.15673	-0.94225
057	0.08975	-0.75902	-0.95415	-1.10049	1.13366	-1.24683	-1.23707
058	-0.11702	-0.54789	-0.89063	-1.15503	0.61742	-1.21378	-1.25295
059	0.27563	-0.27563	-1.26792	-1.37818	-1.26792	-0.60640	-0.71665
060	0.86052	-0.73907	-0.94643	-0.20587	-0.32436	1.12712	1.83806
061	0.03913	-0.57752	-0.55380	-0.22175	0.01541	-0.26919	-1.45506
062	-1.32040	-0.71295	1.30122	0.72574	0.88560	-0.29733	-1.19252
063	-1.37920	1.32511	-0.02704	-1.37920	-1.10876	0.51381	-0.02704
064	1.69083	-0.04455	-0.32597	0.23685	-0.98260	-0.51358	0.47137
065	0.80451	-0.25405	1.83283	0.98597	-1.61507	0.59279	0.86500
066	1.06538	-0.68321	-0.82742	-1.33217	1.49802	-1.04375	-1.40428
067	0.70673	-1.21279	-0.75472	-1.45273	1.44837	-1.19098	-1.53998
068	0.62268	-2.53391	-0.77501	-0.90065	0.29288	-0.85353	-0.74360
069	0.04716	-2.07703	-0.92675	-1.38686	-0.17522	-0.63534	-1.04944
070	-0.79013	3.54531	-0.22652	0.03359	-0.71643	0.03359	0.51049
071	0.10577	-1.08185	-0.95814	-1.10659	1.04597	-1.13133	-0.99525
072	-1.54900	1.20842	-0.15489	-0.12314	-0.51030	0.29965	0.33140
073	0.78695	-0.56670	-0.61258	0.16748	-1.94330	-1.78270	-0.31432
074	0.50821	0.94813	0.20396	0.64183	-0.24417	0.69322	0.92757
075	0.71483	-0.79008	-1.19856	0.52134	-2.16600	-0.48909	0.67183
076	1.01109	-1.69905	-0.65668	-1.38634	-1.17787	0.12508	-0.23974
077	-0.16699	-1.44857	-1.05050	-1.21555	1.02720	-0.68156	-1.08934
078	-1.01746	0.06701	-0.69007	-0.69007	-0.51614	-0.73099	-0.73099
079	-0.45569	0.18387	-0.25582	-0.21585	0.06395	0.26382	0.30379
080	-1.42477	1.22152	-0.41886	-0.50656	-0.68710	0.09697	0.00928
081	-1.47451	1.93059	-0.29820	-0.18814	-0.37387	0.75428	0.65797
082	-0.12734	-0.12734	-0.12734	-0.12734	-0.12734	-0.12734	-0.12734
083	-1.42523	1.41576	0.15084	-0.24824	-0.49852	-0.41735	-0.56616
084	-1.09405	-0.16502	-0.92291	-0.62954	0.64176	-0.28726	-0.09168
085	-1.07114	0.00000	0.42845	2.35651	1.71382	0.21422	0.64268
086	-0.81731	3.02887	1.10577	0.14423	-0.81731	1.10577	0.14423
087	-0.84325	1.18055	1.18055	1.85515	-0.84325	1.18055	1.85515
088	-0.40944	2.32020	-0.40944	-0.40944	-0.40944	-0.40944	-0.40944
089	-0.32489	-0.32489	-0.32489	2.92403	-0.32489	-0.32489	2.92403
090	0.53076	0.13918	-0.42265	1.32243	-0.39711	0.34348	1.14367
091	0.58285	0.41711	-0.68782	-0.68782	-0.13535	-0.13535	0.96958
092	-0.30420	-0.81122	0.87882	3.41390	-0.30420	-0.30420	0.87882

093	-0.24422	-0.35607	-0.24422	0.01677	-0.24422	-0.24422	0.01677
094	0.47030	2.21219	0.47030	-1.27157	-0.22644	-0.22644	-1.27157
095	-0.05861	1.99293	-0.05861	-0.93785	-0.05861	-0.05861	-0.93785
096	-0.38229	-0.52432	-0.40596	-0.43752	-0.38229	-0.32706	-0.34284
097	0.88582	-0.13155	-0.79811	0.21926	-0.86828	0.11401	1.58746
098	0.41203	0.13268	-0.07681	-0.91484	1.73891	-0.98468	0.90088
099	0.99546	-1.79846	0.27111	0.99546	0.76781	0.12624	1.24381
100	0.55172	-0.15897	-0.38340	0.10286	-0.34599	1.03799	2.23495
101	-0.63719	0.11911	-1.31787	-1.58258	0.98887	0.04348	-1.65821
102	-0.51133	0.54408	-1.45757	-1.23920	-0.32936	0.39851	-2.29462
103	-0.32201	-0.01533	-1.05038	-0.97371	0.48302	-0.36035	-2.23877
104	-0.21770	0.04707	1.92990	1.22384	-0.15886	-0.12944	-0.04118
105	-0.35234	-0.08389	0.15100	0.98991	-1.69459	0.98991	-1.02346
106	0.36867	-0.08384	1.61976	1.19386	0.23557	-0.40327	1.16724
107	-0.13110	0.13110	1.27828	0.81941	-0.16388	-0.45887	0.26221
108	-0.45624	-0.45624	-0.51002	-1.12851	-0.23215	-0.59966	-1.12851
109	-1.34649	0.91163	-0.45199	-0.79958	-0.76069	0.12165	-0.07766
110	-0.88731	0.04143	1.01305	1.08449	3.04202	0.38436	0.42722
111	-0.08362	0.80839	1.21724	1.73759	-1.04998	0.80839	1.47741
112	-1.23448	0.93066	-0.65245	-0.69901	-0.67573	0.02269	-0.02386
113	0.17530	1.83221	0.52316	0.79778	-1.21613	0.95340	0.84355
114	-0.61513	0.10206	0.04689	2.41916	-1.11165	-0.00827	2.25365
115	-0.14803	1.66990	0.21555	1.66990	-0.40773	0.21555	1.66990
116	-1.20993	-1.45007	-0.44485	-0.54680	0.59997	0.03711	-0.14657
117	-1.44509	1.79055	-0.51274	-0.60236	0.53248	-0.08879	-0.23011
118	-1.37007	2.66611	-0.21184	-0.49269	0.04523	0.38511	0.11809
119	1.33243	0.37975	-1.12866	-0.07012	-0.36122	0.64438	1.59707
120	-0.71897	-0.21443	-1.22351	-1.43374	1.50942	-0.59283	-1.55987
121	-0.40210	0.27819	1.49299	1.34721	-0.83943	-0.40210	0.05952
122	0.24638	0.03057	0.33630	-0.32911	-0.81469	-0.22120	-0.05934
123	-0.88162	-0.26831	1.83224	1.89357	-0.65163	-0.29898	-0.42164
124	0.26315	0.19857	-0.41490	0.74747	0.10170	0.26315	0.42459
125	0.42803	2.30150	-0.11839	0.98747	0.55813	-0.28752	1.98925
126	-0.67155	-0.59263	1.99571	0.40166	-0.76624	0.08601	-0.40324
127	-0.78872	1.99355	0.55458	0.57537	-1.30026	0.91224	0.89145
128	0.62013	-1.53279	-0.73714	-0.87755	1.69660	-1.01796	-1.01796
129	-0.82857	1.52584	0.71085	0.75612	-1.28134	1.02779	0.98251
130	0.28155	-1.03372	-0.78711	-0.78711	2.66549	-0.86931	-0.86931
131	0.58921	-1.82443	-0.54661	-0.68859	1.44108	-0.83057	-0.83057
132	-0.46685	-0.48390	-1.13195	-0.64591	0.08740	-1.20870	-0.63739
133	0.81945	-3.08430	-0.25744	-0.29109	-1.50261	0.24735	0.31465
134	1.30694	0.04607	-0.34189	0.09456	-1.45728	-0.43888	0.57951
135	0.88903	0.22176	1.04603	0.33952	-1.30901	0.26101	-0.01373
136	1.71064	-0.34212	-0.03801	0.41815	-1.33050	-0.49418	0.19007
137	1.59878	-0.12670	-0.04128	-0.02420	-0.92966	-0.51964	0.12955
138	1.35039	-0.04857	-0.47603	0.10686	-0.74806	0.49546	1.81671
139	-0.64240	-0.50680	-1.28651	-0.98140	0.57799	-0.06610	-1.59161
140	1.06886	0.31437	-0.96826	-0.28922	-0.81736	0.28922	0.66646
141	-0.45599	-0.37308	-1.32653	-1.36798	1.01562	-0.45599	-1.05708

142	0.09253	0.05397	1.06924	-0.01028	-0.94844	1.68611	0.77366
143	-0.50864	0.60507	0.30627	1.43358	-1.43222	0.56433	0.71373
144	-0.26424	-0.09735	0.44041	0.47749	0.34769	-0.39405	0.49604
145	0.46770	2.86044	-1.03523	-0.93256	-0.93256	-0.36219	-0.93256
146	0.00000	2.17944	0.00000	-2.17944	0.00000	0.00000	-2.17944
147	-0.01517	0.87219	0.59197	0.49856	-2.63058	0.68537	0.45185
148	-0.24922	0.97090	0.80129	0.69186	-1.66633	0.74110	0.76299
149	0.11614	0.58073	0.34844	0.50330	-1.20018	0.96788	0.81302
150	-1.23870	0.89249	-0.38072	-0.89496	-0.76846	0.22425	-0.28998
151	0.76666	-1.34249	-1.00770	-1.00770	1.00101	-1.00770	-1.00770
152	-0.84795	-0.31441	-1.34339	-1.19095	-0.64470	-0.64470	-1.14013
153	-0.08882	1.79529	0.28800	1.52613	-0.35798	0.28800	1.52613
154	-1.40908	1.65527	-0.15217	-0.14179	-0.77544	0.47108	0.52301
155	0.42118	0.40292	0.26045	0.39561	0.12164	0.27872	0.28602
156	1.06884	-0.54102	-0.51902	-0.17154	-0.41786	-0.59380	-0.23312
157	-1.67669	1.73820	-0.23437	-0.27679	-0.72221	0.40193	0.44436
158	-0.90725	-0.03279	-1.12586	-1.12586	0.07651	-0.03279	-0.03279
159	-1.07068	0.21929	-0.51783	-0.51783	-0.51783	-0.51783	-0.51783
160	0.97327	-0.26441	-0.48945	0.03563	0.29817	0.89826	1.53586
161	-0.37429	-0.01401	-0.93472	-1.09485	-1.01478	-0.77460	-0.97475
162	-0.45622	-0.18048	0.82220	1.14807	-0.35595	0.07018	0.09525
163	1.19379	-0.14137	-0.25917	0.05497	-0.37698	0.32986	1.66503
164	-0.57547	-0.13587	-1.09499	-1.25484	0.14386	-0.01598	-1.37473
165	-0.45745	-0.16058	0.78402	1.37777	-0.45745	-0.10660	0.16328
166	-0.57491	-0.24949	0.50983	2.19120	-0.68339	-0.35796	-1.33424
167	-0.27003	-0.24613	-1.03472	-1.32148	0.30348	-0.19834	-1.01082
168	0.05234	-0.43316	-0.64557	-0.70626	-0.08420	-1.04005	-0.56971
169	-0.39185	-0.09234	-1.09070	-1.46508	0.45674	0.30699	-1.09070
170	0.06030	-0.73315	-0.92358	-1.28540	1.11401	-0.70776	-0.62524
171	1.20668	0.46365	-1.14130	-0.30910	-0.24965	0.58253	1.91999
172	-0.78418	-0.38074	-1.38934	-1.49020	0.77914	-0.63289	-1.99450
173	-0.61211	-0.64253	3.18985	1.33449	-1.09876	-0.36879	-0.04942
174	-0.56198	-0.05226	1.55462	0.22418	0.11187	0.07732	-0.46694
175	0.42292	-0.38441	0.39808	0.48502	-0.50862	-0.47136	0.28629
176	0.01190	0.48828	-0.33213	1.04405	0.25009	0.35595	0.11777
177	-1.35355	0.74212	-0.51415	-0.63433	1.59748	-0.11229	-0.14046
178	-0.16966	-0.13110	-0.13110	-1.28791	-1.10796	-0.85089	-2.40615
179	-0.40064	-1.02910	-0.61489	-0.78628	-0.70059	-0.74343	-1.45759
180	-0.35871	-0.60782	-1.23889	-0.80710	0.63771	-1.02300	-0.42514
181	-0.31317	-0.87575	-1.06328	-0.59446	0.36192	-0.87575	-0.29441
182	-0.00562	0.55692	0.55692	0.89445	-0.56817	1.00697	1.00697
183	-0.19304	0.89964	0.53541	0.82679	-0.92149	1.04533	1.11817
184	0.04432	-0.39896	-1.21166	-1.13777	1.30031	-1.50718	-1.06389
185	-0.27389	-0.70049	-0.91379	-0.94287	0.69564	-0.86531	-0.87501
186	1.11278	-0.76567	-1.01069	-0.07146	-0.31647	0.33689	2.13368
187	-0.18250	-1.15364	-0.98620	-0.38343	0.38678	0.55421	-2.29221
188	-0.87601	1.23195	1.40473	0.22980	0.12613	-0.56500	-0.77234
189	1.42335	0.40990	-0.31807	0.06732	-1.51708	-0.48460	0.52409
190	1.60884	1.08001	-0.28949	-0.42509	-0.33017	-0.24881	0.61899

191	0.22562	-0.93828	0.07632	-0.88039	-1.20946	-0.82250	-0.72195
192	-0.70327	-1.26980	0.26372	-1.44562	-0.44931	-0.81072	-1.25027
193	0.24696	-0.97100	-0.17399	-0.92610	-1.09168	-0.75772	-0.67353
194	-0.60329	-1.22206	-0.09625	-1.43690	-0.37125	-0.72361	-1.11893
195	0.13420	-0.75472	0.79572	-0.66514	-1.42658	-0.92699	-0.79262
196	-0.91562	-1.15748	1.36479	-1.18051	-0.58162	-0.92713	-1.41086
197	1.64066	-0.40100	-0.49748	-0.42801	-1.51639	-0.70589	-0.07680
198	0.57171	-1.17412	-0.59857	-1.15493	-0.69449	-0.73286	-0.90553
199	1.13108	-0.82860	-0.79579	-0.83516	-0.76955	-0.74986	-0.84172
200	0.30919	-0.88149	-0.60687	-0.84693	-0.80083	-0.72978	-0.64720
201	0.78995	-1.05708	-0.55335	-0.52282	-1.10288	-0.73652	0.62204
202	1.45660	0.70252	-0.32830	0.49796	-1.59177	-0.09566	1.13170
203	1.99081	0.34153	0.25348	0.38217	-1.46013	-0.10887	1.46927
204	0.07720	-0.31648	-0.09663	0.38396	-0.89933	-0.28069	1.04862
205	0.01982	-0.61368	0.45506	0.12621	-1.35359	-0.24131	0.51793
206	0.80112	-0.80243	-0.66349	-0.75993	-0.40031	-0.67493	-0.80407
207	0.76811	0.74988	-0.23446	-0.01572	-1.50592	0.17567	1.25573
208	0.04802	-0.15006	0.45020	0.57626	-1.23057	-0.45621	0.62428
209	0.87763	-0.95232	-0.54163	-0.81743	-0.49130	-0.77717	-0.81743
210	0.16993	-0.39458	-1.17799	-1.39689	1.95565	-0.75173	-0.95910
211	-0.19707	-0.39250	-0.86592	-1.27054	1.14612	-0.89620	-1.13842
212	-0.28280	-0.75415	-0.75415	-0.75415	-0.75415	-0.75415	-0.75415
213	-0.71369	1.40096	0.97299	1.18446	-1.41858	1.16935	1.09886
214	-1.61600	2.21293	0.17559	0.30243	-1.30683	0.66709	0.29450
215	0.40587	-0.00687	1.12001	1.29036	-0.76687	0.96932	1.19208
216	0.43420	-0.41312	0.05698	0.09916	0.09087	-0.09478	-0.11059
217	0.34332	-0.28309	-0.14073	-0.11496	0.10773	-0.26557	-0.35075
218	0.34150	-0.49440	-1.07310	-2.55916	0.32007	-0.36579	-0.43009
219	0.21362	-0.03731	0.95358	1.48764	0.03989	0.31014	0.76698
220	0.42650	-1.11184	1.08031	-0.18114	0.22652	-0.78879	0.44189
221	-0.10255	0.63426	0.59332	1.55674	-0.19611	0.52315	0.85209
222	-0.02483	0.49764	0.34678	-0.65033	-1.98596	-0.17201	0.19960
223	1.18978	-0.33083	-0.45413	0.03904	-0.37193	0.12123	1.72406
224	1.18218	0.13633	-0.98421	-0.12512	-1.13362	0.92072	1.77981
225	-0.82840	0.07381	-0.82840	-1.23850	0.44290	0.07381	-1.73062
226	-0.30400	-0.72428	-0.52815	-0.72428	0.31240	-0.16390	-1.59285
227	-0.31635	-0.12708	1.41413	0.87335	-0.72193	0.11626	-0.47858
228	-1.01719	-0.21715	1.26863	1.32577	1.21148	-0.18858	-0.73146
229	0.65056	-0.70478	0.37949	-1.33727	1.91556	-0.52406	0.74092
230	1.13241	-0.27086	-0.53194	0.21865	0.90397	0.44709	2.27462
231	0.55017	0.16028	-0.66280	-0.09963	0.03032	1.76315	1.50323
232	-0.56354	0.09263	-1.41271	-1.25832	0.01543	0.09263	-1.21972
233	-0.71595	-0.15891	0.75854	-0.19168	-1.07638	-0.09338	-1.63341
234	-0.08082	0.10286	-1.25644	-0.96254	0.02939	-1.36666	-1.51361
235	-0.30543	-1.12071	0.67526	1.73866	-1.12071	0.58073	-0.37632
236	-0.12383	0.89045	1.03198	0.74892	-0.21819	0.32433	-0.02948
237	-0.09165	-0.45826	0.98200	-0.11784	-1.16531	0.30114	-1.08675
238	-0.08247	-0.13099	1.49432	0.64527	-0.81023	-0.71320	-0.08247
239	0.17686	0.50847	0.95062	1.42435	0.06632	0.79271	1.07695

240	-0.38850	-1.01561	-1.18385	-1.13797	0.22331	-0.78618	-0.46497
241	-0.17733	-0.71307	-1.04536	-1.06571	1.61976	-0.85548	-0.91651
242	-0.17176	-0.68802	-1.09592	-1.08955	1.93786	-0.77724	-0.96208
243	-0.15826	-0.66696	-1.17566	-1.11914	1.90480	-0.66696	-1.06262
244	0.69901	-1.12851	-0.38825	-1.35985	1.34674	-1.11309	-0.14920
245	0.24423	-0.80194	-1.91735	-0.38654	1.24426	-1.74042	-0.53270
246	-0.82115	-0.55342	-0.69433	-1.14525	1.63068	-0.08842	-0.08842
247	-0.09205	-0.72193	-0.94266	-0.68425	-0.45275	-0.63041	-0.30740
248	-0.11737	-0.49084	-1.19508	-1.29112	1.81397	-0.75760	-1.13106
249	0.21817	-1.37973	0.56644	0.83276	0.91470	0.23866	-0.25300
250	1.61088	-0.75655	-0.57641	0.71023	-0.98814	-0.49922	0.58156
251	1.06109	0.25097	-0.59256	0.60174	-2.48006	-0.27519	0.91076
252	-0.60720	2.23472	0.70144	1.59992	-0.69021	0.55984	1.39484
253	0.97327	-0.26441	-0.48945	0.03563	0.29817	0.89826	1.53586
254	-0.37429	-0.01401	-0.93472	-1.09485	-1.01478	-0.77460	-0.97475
255	-0.42680	-0.17720	0.82115	1.14562	-0.37688	0.04742	0.12229
256	0.72540	0.14508	-0.43524	-1.01557	0.14508	0.33852	0.33852
257	-0.47007	-0.72648	-0.81195	-0.89742	0.29914	-0.47007	-0.72648
258	1.34667	0.64482	-0.58341	0.38163	-1.89938	0.03070	0.11843
259	1.68950	-0.64084	0.00000	1.04865	-0.69910	-0.58258	1.39820
260	2.25271	-0.36425	0.30767	1.15641	0.09548	-0.82399	1.79297
261	1.05238	-0.09112	-0.12685	0.40916	-0.16259	0.94518	1.01665
262	1.88316	-0.57135	-0.21681	-0.02590	-0.38045	-0.38045	1.22862
263	1.21720	0.87149	-0.71303	0.41053	-0.28089	0.26648	0.81387
264	1.50330	0.72355	-0.62952	-0.85886	-0.14792	0.54008	0.79235
265	0.64360	0.22662	-0.29914	-0.75238	-0.00906	0.38979	0.42605
266	0.36428	0.25150	-0.08684	-1.53042	-0.13195	0.34172	0.36428
267	0.72339	0.45811	-0.11325	-1.56207	-0.43974	0.92744	-0.03162
268	0.49466	0.13860	-0.14115	-1.51450	-0.34460	0.29120	-0.62436
269	0.57167	0.66218	-0.06184	-0.93670	-0.84620	-0.78587	-0.72553
270	-0.23271	0.31733	-0.23271	-0.90969	-0.95200	-1.07894	-0.69813
271	-0.64380	-0.43612	1.26684	0.31151	-0.97609	0.97609	-0.14537
272	-0.10589	0.01176	1.54133	-0.41965	-1.12560	-0.02745	0.28630
273	-0.58085	0.58085	0.52805	0.10561	-1.10890	0.52805	-0.10561
274	-0.35191	0.66918	-0.82600	-0.20604	-2.17532	-0.24251	-1.26361
275	-0.90874	0.71712	-1.54748	-1.57651	-0.18291	0.19452	-1.51844
276	-0.17092	0.36494	-1.63070	-1.63070	0.25407	-0.06005	-0.61440
277	-0.28271	0.08569	-1.11563	-1.50006	0.32596	-0.07448	-0.87536
278	-0.32803	-0.00754	-0.47885	-0.87475	1.04819	-0.45999	-1.25180
279	0.21362	-0.21631	-0.99558	-0.21631	1.04664	-1.72112	-0.86123
280	-1.30285	-0.09361	0.60852	-0.36667	0.92058	-1.84896	-0.67873
281	-0.90536	-0.09631	0.52010	0.78978	-0.13484	-1.52178	0.09631
282	0.01740	0.27840	0.23490	0.58290	0.01740	-0.63510	0.53940
283	-0.15982	0.10111	0.36204	0.81867	-0.58383	-0.09458	-0.09458
284	-0.55229	0.03468	-0.28548	0.51494	1.31536	-0.71238	-0.39220
285	-1.01163	0.55476	-1.83835	0.20667	1.59903	-0.01087	-1.05514
286	-1.77138	0.26373	0.01453	-1.27298	0.80366	0.59599	-1.68831
287	-0.45924	0.03061	1.01033	-0.78581	2.03087	-0.86746	-0.58170
288	-0.63137	0.26026	1.44108	1.41698	0.40485	0.18796	-0.31809

289	-0.43301	-0.64266	1.14745	0.87328	0.00241	-0.12659	-0.19110
290	-0.51393	-0.27253	1.04883	1.22671	-0.20900	0.00698	-0.09465
291	-0.28400	-0.01157	0.65586	0.92828	-0.47470	0.05652	0.13825
292	-0.24667	0.40491	0.66555	1.24268	-0.15358	0.21874	0.12566
293	0.16244	-0.16244	-0.11603	1.94935	-0.58016	-0.16244	0.34809
294	-1.00940	-0.24553	-0.35465	1.68234	0.19096	0.95484	0.73659
295	-0.88275	-0.78645	0.04815	0.94695	0.46545	1.36425	0.75435
296	0.11317	-0.25060	-0.45270	-0.04850	1.28537	1.72999	1.24495
297	0.02624	0.31437	0.56133	0.64366	-0.32363	1.18905	0.56133
298	-0.21752	0.92347	0.42970	0.64990	-0.71795	1.17702	0.84340
299	-0.35784	0.17159	0.40794	1.06028	-0.98181	2.20423	0.81447
300	-0.99105	1.77963	-0.92001	0.54821	-0.87264	1.04551	1.23496
301	1.82032	0.14471	-1.26432	-0.46460	-0.23610	0.52553	1.47758
302	-0.36614	1.18746	0.72487	1.22237	-1.08185	-1.08185	1.20492
303	-0.83414	0.92864	0.14720	0.01999	3.45471	-0.56155	-0.54337
304	-0.92233	-0.63369	-0.55497	-0.18761	-0.24009	-0.79113	-0.58121
305	-1.28236	-0.42171	2.20326	0.09467	-0.67991	-0.32130	0.19508
306	-1.12860	-0.04989	0.00404	0.47598	2.35025	-0.99376	0.03101
307	1.19512	-0.19666	-0.28743	0.31769	-0.68076	1.01358	1.04384
308	-0.57590	-0.57590	1.80594	0.66104	-0.57590	-0.57590	-0.57590
309	-0.25120	-0.28645	0.26001	1.05328	-0.19831	-0.19831	-0.58613
310	-0.71104	1.05162	-0.74091	-1.69693	-0.26290	-0.68116	-1.30855
311	-0.44144	0.03450	-0.06068	0.01070	2.72366	0.81983	0.43906
312	-0.66377	-0.02706	2.02861	-0.32722	1.12357	-0.91088	-0.19836
313	-0.85176	-0.49020	-0.95506	-0.27480	0.91099	-0.01104	-0.44953
314	0.66173	-2.52046	-0.94553	-1.34116	0.56092	-0.73630	-0.97786
315	-0.08793	-1.88573	-0.60578	-0.59601	-0.59601	-0.66440	-1.36789
316	1.44628	-0.87810	0.00996	0.37697	0.24557	-0.35250	-0.16673
317	0.75637	-2.76644	-1.11741	0.45117	0.45117	-0.84296	-0.97309
318	1.10090	-2.48198	-0.88382	0.84677	0.84677	-0.81939	-0.84445
319	-1.06503	1.29701	-0.27215	-0.32792	-0.43947	0.20115	0.27954
320	0.54471	-2.64709	-0.62912	-0.41810	0.92720	-1.09075	-0.25982
321	-0.24880	-1.13698	-0.72705	-1.09143	1.36814	-1.01172	-1.05727
322	-0.65424	-1.34291	0.49355	0.95266	-0.88380	0.03443	0.03443
323	-0.65424	-1.34291	0.49355	0.95266	-0.88380	0.03443	0.03443
324	-0.49507	-0.60758	2.88041	1.30518	-0.38255	-0.60758	-0.60758
325	0.27964	-0.49714	-0.49714	-0.34178	-0.34178	-0.49714	1.83322
326	1.05204	-0.17534	-0.52602	2.80545	0.35068	-0.35068	1.75340
327	0.00707	-0.84192	-0.41742	1.70506	-0.55892	0.71457	3.26156
328	0.00000	0.49002	-1.34757	-0.98005	0.00000	0.24501	-0.73504
329	0.79582	0.35369	0.35369	-0.97267	1.23794	0.79582	-0.30948
330	2.03925	0.67975	-0.40785	-0.13595	-0.95165	0.67975	-0.67975
331	1.01622	-0.12081	-0.68933	-0.54720	-1.54211	-0.12081	0.02131
332	0.22950	-0.39078	-0.63889	-0.76295	-0.51483	-1.13512	-0.51483
333	-0.46156	-0.29672	-0.29672	-0.62641	-1.28579	0.52750	1.02203
334	0.61005	1.73383	-0.19264	-0.51372	0.28897	0.93113	1.09167
335	0.03120	-0.09360	0.15600	-0.84245	0.65524	1.27927	-0.34322
336	-0.09889	0.02472	0.89009	-0.22252	-0.59339	0.02472	-0.71702
337	0.06273	1.06645	-0.18819	1.06645	-0.43912	1.06645	-0.43912

338	-0.56163	0.08953	0.74070	0.57791	-1.05000	0.08953	-0.56163
339	1.51729	-0.18391	-1.14946	0.13793	-0.27587	0.25288	1.81616
340	0.61293	-1.03769	0.17276	1.73535	0.28280	-0.04731	2.37359
341	1.16734	0.20209	-0.76314	-0.31068	-0.58216	0.24734	0.48865
342	0.43031	0.29745	-0.39636	-0.55875	0.99128	0.48936	0.45984
343	-0.65058	0.08592	-1.14158	-1.22341	1.17704	0.30414	-1.38708
344	-0.58336	0.12305	-0.92518	-0.97076	0.87505	0.21420	-1.81391
345	-0.14668	0.20031	-0.77760	-0.96688	1.55679	0.61041	0.83123
346	-1.30063	0.54811	1.09492	0.80850	1.14700	0.10545	-1.22251
347	-1.19874	-0.07171	1.77250	1.26021	-0.17417	-0.20832	-0.68645
348	-1.02192	0.52539	0.96419	0.50230	1.49536	-0.39837	-0.90645
349	-1.12905	0.26374	-0.21040	-0.21040	1.15276	0.97495	-1.30685
350	-0.62775	-0.22574	1.56785	0.14534	-1.30809	-0.00927	-1.21531
351	-1.26048	0.66716	1.19288	0.79233	0.96757	0.06634	-1.28551
352	-1.11160	-0.28584	-0.92104	-1.23864	0.85752	-0.53992	-0.92104
353	-1.11578	0.68875	-0.71716	-0.84844	-0.02494	-0.33763	-0.46414
354	0.03035	-0.83683	-0.92355	-1.01027	1.50456	-1.01027	-1.01027
355	-0.60003	2.13900	1.09443	1.41402	-0.52925	0.91426	1.12017
356	-0.20316	1.89521	1.14973	0.82761	-0.81519	1.08070	0.92425
357	-0.64120	-0.94653	0.88546	0.58013	-0.33586	0.27480	2.10680
358	-0.50789	-0.50789	-1.17369	-0.67884	-0.53488	-1.25466	-0.66984
359	0.50460	-0.27170	0.78185	-1.38072	-0.02218	1.08683	-0.93711
360	1.44333	-0.76209	-1.01053	-1.61201	0.32754	-1.10206	-1.77763
361	-0.49682	0.32721	-0.61018	-1.25982	-0.81946	-0.30934	-1.08978
362	-0.29523	-0.75279	0.69832	-0.36931	1.63087	-0.13399	-0.82687
363	0.77988	0.56229	-0.86348	-1.45898	-0.07329	0.24163	0.20155
364	-0.60345	-0.89264	-0.89264	1.66614	0.05545	0.31170	-0.67667
365	-0.40061	-0.59066	-0.92076	-1.31087	0.16954	-0.91076	-1.22085
366	1.41461	0.18004	-1.02023	0.00857	-0.95164	0.04286	2.13477
367	-0.20355	0.08441	-1.01684	0.37396	-0.93931	0.85497	-0.59596
368	-0.93587	0.23053	-0.77092	-1.95697	0.94137	0.03809	-1.51318
369	0.38166	-0.29440	-0.52484	0.14783	-0.49265	0.54433	-0.06904
370	-0.97947	-0.62569	2.11607	0.98792	0.69310	-0.55886	-0.67679
371	-0.18828	2.00486	0.20971	1.76829	-0.00180	0.20414	-0.90634
372	-0.54968	0.38291	1.91216	-0.01286	0.71372	1.23088	-0.55310
373	-0.79138	1.19200	0.52711	2.64686	-1.16101	-1.16101	-1.16101
374	0.08240	-1.30743	0.69719	0.96750	0.05131	-0.49409	0.24746
375	-0.54184	-0.19202	1.35610	1.40820	0.16523	0.03870	-0.85445
376	-0.45587	1.55221	0.30495	1.46490	-0.15653	0.80385	0.15528
377	0.45269	0.23073	-0.56459	-0.86053	0.84573	-0.12068	0.16600
378	-0.65132	-0.47224	0.50499	-0.01688	-0.50806	-0.25735	-0.41085
379	-0.29039	1.16647	-1.12842	1.92125	0.84314	0.67265	-1.07350
380	-0.63807	-0.63807	-0.63807	-0.63807	-0.63807	-0.63807	-0.63807
381	-0.73169	2.59136	0.32413	1.55367	0.30469	0.18867	1.13821
382	1.74458	-0.78322	-1.14341	-1.05827	0.99147	-1.28748	-1.31367
383	0.54971	0.49608	0.54971	0.44245	0.33519	0.17430	0.28156
384	-0.25409	-0.40504	-0.75725	-1.00882	1.30569	-1.10945	-0.95851
385	1.00209	0.03492	3.33941	-0.07253	0.24985	-0.90537	-0.63671
386	0.14676	-1.33508	1.68560	-0.90763	-0.82214	-0.45167	0.11826

387	0.48810	-0.47930	-0.97767	-1.65192	1.19167	-0.06889	-1.15356
388	-0.19294	0.66006	1.02563	2.24420	-0.80222	0.45696	2.04111
389	1.14702	-2.51180	-0.79788	-1.01044	0.61477	-0.74766	-0.88491
390	0.02249	0.95891	1.07221	1.21218	0.23577	0.72564	1.02556
391	-0.81200	1.18107	0.67929	0.52922	-0.45559	0.24784	0.18219
392	0.04964	-1.94184	0.47276	1.33029	2.32885	-0.64427	-0.04061
393	-0.25595	-2.70050	-0.34223	-0.25595	0.46302	-0.88866	-0.16968
394	-0.24022	-3.08112	-0.49089	-0.15666	0.38644	0.47000	-1.03400
395	0.25207	-4.22488	0.10102	0.07379	0.27436	0.21493	0.27188
396	0.28203	-4.21306	0.20453	0.13187	0.10765	0.26992	0.13913
397	-0.24418	0.19597	-0.60050	-1.66246	0.81778	-0.44679	-2.05371
398	-0.42711	-0.42711	-1.13658	-0.60927	0.19606	-1.22287	-0.59969
399	-0.83482	-0.23474	-0.54989	-0.79597	-0.41174	-0.19804	-0.38800
400	-0.62033	1.75257	-0.46609	1.64761	-0.55279	-0.45924	1.65674
401	-0.01497	2.67551	-0.34846	-1.84067	-0.55194	-0.21280	-1.58631
402	-0.02663	-0.96784	-0.82577	-1.28749	-1.28749	-0.18646	-1.21646
403	-0.29776	0.80898	-1.08830	1.01979	-2.08965	-0.29776	2.17924
404	-0.05947	0.76795	0.30252	0.30252	-3.00717	-0.47318	0.25081
405	0.26492	-0.90171	-0.41561	1.91765	-1.92251	-0.61005	0.55658
406	-0.83971	-0.29679	0.93382	2.67116	-1.16546	0.35470	0.42709
407	-1.00832	-0.68537	1.18056	2.25707	-2.08483	0.35524	-0.03947
408	0.20123	0.08286	-0.69840	0.29593	-1.78743	0.69840	3.04219
409	0.91553	-0.17027	-0.86124	1.53247	-1.23140	1.43376	2.59360
410	0.89088	0.67465	-1.01197	-0.25515	-1.07684	0.89088	1.47472
411	1.01265	0.69742	-0.85898	-0.83927	-0.87868	0.77623	0.59892
412	1.69420	1.55036	-0.50446	-0.15513	-0.87432	-0.01130	1.55036
413	1.29221	1.22002	-0.96975	0.13716	-1.73979	1.02751	1.86973
414	0.99771	0.82229	-0.80036	-0.20831	-1.45820	1.06350	1.12928
415	1.31413	0.39292	-0.62228	-0.65988	-0.75389	-0.28388	0.24252
416	0.59229	0.70843	-0.74327	-0.82069	-1.13039	0.66972	0.78585
417	1.63951	1.25504	-0.50256	-0.11808	-1.17997	0.48608	1.65782
418	0.43847	1.05974	0.77300	-0.68459	-1.35365	1.01195	0.62963
419	-0.36825	0.29246	0.83658	-0.32938	-1.00953	-0.01846	-0.07675
420	-0.46246	-0.30299	-1.04718	0.70698	-1.84453	0.01594	0.28172
421	0.30710	0.90054	0.12907	0.54447	-2.15566	0.27743	0.95988
422	-0.79659	0.34871	-0.07323	1.37346	-0.97743	-0.31435	0.65011
423	0.99843	0.92812	0.01406	-0.19687	-0.26718	0.57655	0.15468
424	-0.78554	-0.66974	0.11516	0.01222	-0.09071	-0.21938	-0.14218
425	-0.10182	0.26567	0.87817	1.18442	-1.29620	0.70973	1.58255
426	0.23488	0.16216	1.18024	1.06389	-1.49585	0.62757	1.12207
427	-0.06135	0.79224	0.68554	0.68554	-1.52847	1.19236	1.48579
428	-0.81306	0.51891	0.07492	1.35140	-0.70206	1.07390	1.57339
429	-0.91777	-0.69528	0.42551	0.32539	0.34485	-0.44219	-1.62974
430	-1.28310	-0.77169	0.51064	-0.08854	0.57934	-0.70681	-1.06937
431	0.67373	0.23012	1.17279	1.46711	-0.80639	0.54577	0.69506
432	0.24101	-0.17386	0.10628	0.36932	-0.62509	-0.00491	0.20679
433	-0.01904	-0.27802	0.30087	0.72744	-0.41513	-0.12568	0.01142
434	-0.14689	-0.35413	-0.45166	-1.43911	0.35292	-0.64671	-2.40217
435	0.56014	-0.16522	0.31835	0.07656	-0.40701	0.15716	0.07656

436	-0.92848	1.23497	1.23497	1.05468	-0.74819	1.05468	1.05468
437	0.67600	0.41652	-0.10242	-0.06145	-0.06145	0.45749	0.08876
438	-0.07219	0.08647	0.97497	1.29229	-0.45297	0.75284	0.91150
439	-0.38153	-0.28188	0.52959	1.09905	-2.11838	1.26989	2.38033
440	1.55057	-0.16122	-0.24084	0.51553	-1.75360	-0.87779	0.75438
441	1.69366	-0.55919	0.04425	0.40631	-1.60516	-0.84080	0.40631
442	2.77921	0.15270	-0.54973	0.21378	-1.49650	-0.39703	1.16055
443	2.69117	-0.35422	-0.41834	-0.12983	-1.34799	-0.06571	0.89598
444	-0.08522	-0.43741	-0.95865	-0.77551	-1.04317	-1.12770	-0.84595
445	-0.88954	-0.26748	1.02640	-0.46654	0.27992	-0.81490	-0.24260
446	0.71631	-1.87484	-0.90048	-0.94331	1.33733	-1.39301	-1.30735
447	0.59038	-1.35430	-0.75593	-0.69609	1.44804	-1.19473	-1.06509
448	0.35723	-1.23994	-0.86726	-0.57977	1.72016	-1.18670	-1.03763
449	0.19644	-1.18959	-0.94949	-0.46928	1.83350	-1.18959	-0.96040
450	0.01182	-1.20618	-1.17071	-0.27198	2.02213	-1.30079	-0.94603
451	-0.23247	-0.94601	-1.17619	0.22787	2.28793	-1.06110	-0.38209
452	-0.43392	-0.75383	-1.21319	1.61677	2.28120	-0.72102	0.54220
453	-0.39031	-0.04406	-0.01259	4.20528	-0.29588	-0.07554	-0.10702
454	-0.29075	-0.99399	0.49361	0.54771	1.35913	-0.23666	-1.07513
455	-0.39581	0.16013	1.01823	1.10283	-1.01219	1.76756	0.84903
456	1.71438	-0.38097	-0.19048	-0.04762	-1.00005	-0.47621	0.04762
457	1.23424	-0.00237	-0.28775	0.09274	-1.33412	-0.43044	0.56837
458	1.29679	-0.16262	-0.53789	-0.49620	-1.24675	-0.78808	-0.16262
459	1.37302	-0.04734	-0.47345	0.23672	-1.46771	-0.28407	0.99426
460	1.30518	1.46291	-0.50866	-0.11435	-1.33673	-0.11435	0.59541
461	-0.13087	0.86028	-0.27423	0.50682	-1.16405	-0.52635	2.85743
462	0.54575	0.57659	0.15405	1.10091	-1.44665	0.07386	2.44563
463	0.71383	-0.14394	1.21029	1.08984	-1.34542	0.12337	0.25263
464	0.06917	0.72317	0.33328	0.91497	-1.25454	0.31442	1.77963
465	1.33874	-0.35354	-0.72655	-0.41113	-1.06391	-0.91580	-0.26851
466	1.73432	-0.50426	-0.62315	-0.47236	-1.02331	-0.78263	-0.43176
467	1.73732	-0.68415	-0.05597	-0.18933	-1.29829	-0.82803	-0.84909
468	0.88111	-0.59461	-0.66489	-0.59461	-0.62975	-0.57840	-0.62975
469	0.84975	0.32365	-0.68943	0.04994	-1.51413	-0.98803	1.70644
470	1.66974	-0.04081	-0.38949	0.29965	-1.66113	-0.56177	1.13647
471	1.60486	-0.54251	0.74338	0.57949	-1.72337	-0.46687	-0.39964
472	0.74915	0.07779	-0.27149	0.22748	-1.45543	-0.21705	0.85802
473	-1.21360	-0.69717	-1.56694	-0.76965	0.17259	-0.20792	-0.76965
474	-0.12594	-0.15064	-0.51283	-0.68570	0.06338	0.51613	0.45027
475	-1.17461	-0.53372	-0.09245	0.03362	0.27526	-0.46018	-0.03992
476	-2.29426	-0.23329	-0.43366	-0.37641	0.63976	-0.24760	-0.89165
477	-1.31914	-0.57733	-0.09907	0.10590	0.34991	-0.32356	-0.02098
478	-1.18394	-1.10542	-0.02355	1.12810	0.31670	-0.41616	0.67441
479	-1.75741	-0.29290	-0.76094	-0.36839	0.66582	0.03170	-0.27025
480	-0.93853	-0.53236	-0.90951	-0.96029	-0.56137	-0.47434	-0.56863
481	-0.62107	0.45905	-0.92486	-0.94737	-1.35242	-0.46355	-0.46355
482	0.76495	-1.54272	-0.34615	-1.20084	0.25213	-1.79913	-0.60255
483	-0.55940	0.68202	-0.55940	-0.55940	-0.55940	0.07397	0.08411
484	-1.32607	1.14890	-0.51496	-0.71100	-1.00261	0.08539	-0.11308

485	-1.34338	1.18786	-0.49882	-0.67893	-1.01967	0.10234	-0.07289
486	-0.29079	1.16567	-1.12839	1.92125	0.84256	0.67355	-1.07371
487	0.20415	-0.28281	-0.79225	-1.25674	1.14062	-0.74730	-1.02450
488	-0.38950	-0.91037	-0.28075	-0.53832	-0.14338	-0.24641	-0.48108
489	0.47527	0.06926	-0.68604	-1.15475	-0.08896	-0.81143	-0.44124
490	-1.00804	-1.54064	-0.20589	-0.24811	2.54479	-0.48843	-0.09223
491	-1.37406	0.19606	0.67826	-0.63283	1.56295	-0.37778	0.07651
492	-0.34998	2.00285	0.88525	1.32641	-1.02642	0.85584	1.62052
493	-0.13810	-0.86854	-0.86854	-0.66310	0.02168	-0.70876	-0.38919
494	0.54690	-1.50253	-0.97365	-1.00670	1.00968	-1.03315	-0.87448
#	G	H	I	L	K	M	F
001	-1.74623	0.82921	-1.82427	-0.96579	-0.22437	0.39997	0.94628
002	-1.12296	-0.46916	1.48013	0.64471	0.18463	0.22096	1.23798
003	-0.54102	-0.74475	0.54555	2.56025	-1.02772	1.92641	1.12279
004	-0.47672	-0.86904	0.77156	2.26950	-1.03548	2.30517	1.19954
005	-0.77607	0.13481	0.60847	1.59222	0.13481	1.59222	0.13481
006	-0.61071	0.53437	1.48862	0.53437	-1.24687	1.48862	1.48862
007	1.16478	0.13150	-1.65324	-0.90176	0.13150	-0.38513	-0.90176
008	1.41260	-1.25109	0.42426	-0.74487	0.47247	-1.58858	-1.35957
009	-2.05947	0.21293	0.62573	0.62573	0.75243	0.44998	1.11209
010	-0.34982	0.24502	1.19867	1.14201	-1.55841	0.94373	1.55747
011	-0.13824	0.39162	0.90222	0.97930	-1.87237	1.10454	1.36466
012	-0.44385	-0.55124	0.48681	2.08566	-0.74215	0.36749	1.99020
013	-0.61872	-0.06675	1.08854	1.60201	-0.64440	0.20281	1.56350
014	0.95135	0.82250	-1.47535	-1.69011	0.57553	-0.62708	-1.55052
015	-1.25010	-0.57538	1.46126	1.87359	0.93648	0.21178	0.79904
016	0.24694	0.25976	0.14220	0.26404	0.25602	0.26137	0.15983
017	-2.32029	0.81826	-1.11828	-0.35034	-0.47913	0.26019	0.97567
018	-0.12706	0.76983	0.39612	0.20927	0.20927	-2.21981	1.29302
019	-1.71868	0.62080	0.37014	0.78790	0.63751	0.76284	-0.06433
020	-0.31322	-1.58891	0.81439	0.68910	-0.84856	0.40434	-0.24488
021	-3.05751	0.20756	1.70017	1.51359	0.11427	0.58071	0.20756
022	-1.80091	0.55590	0.10503	0.10503	0.44318	0.46367	1.17072
023	-0.75127	-0.44061	0.02745	0.19255	-0.44061	-0.05242	0.18663
024	1.70378	0.23359	-1.10590	-1.00789	-0.02777	-1.33460	-0.94255
025	0.17720	0.36577	0.87603	-0.68801	-0.22212	-1.83054	-0.31641
026	-1.77951	0.00000	1.77951	0.00000	0.00000	0.00000	0.00000
027	-1.22540	0.52517	0.52517	2.27574	0.52517	0.52517	0.52517
028	-0.86438	0.95537	-0.86438	-0.86438	0.95537	0.95537	0.95537
029	-1.41305	0.39084	-0.21045	-0.21045	0.99214	0.39084	0.99214
030	1.94935	-0.48733	-0.48733	-0.48733	-0.48733	-0.48733	-0.48733
031	-0.97467	0.97467	-0.97467	-0.97467	0.97467	0.97467	0.97467
032	-2.01233	0.36467	0.40001	0.37881	0.45891	0.44713	1.21512
033	-2.17994	0.56644	0.10871	-0.00572	0.68087	0.33757	0.90974
034	-0.89503	-0.03648	-1.10967	-0.89503	2.28159	-0.55161	-0.85211
035	0.49656	-0.58789	1.86641	1.01026	-1.38696	0.72487	1.29564
036	1.20155	-0.91107	1.33359	0.93747	-1.17515	0.27728	0.67340
037	1.54899	-0.11307	-1.42093	-1.09397	0.05040	-1.06672	-1.06672
038	-1.52976	0.00000	0.28460	0.74709	0.56921	1.60092	0.46248

039	-0.75620	-0.43037	1.55178	0.73719	-0.78335	0.05837	0.95442
040	1.54899	-0.11307	-1.42093	-1.33919	0.54085	-1.06672	-0.90324
041	-0.44225	-0.49543	-0.60178	-0.76131	-0.61951	-0.53088	-0.70814
042	-1.26503	1.65177	-0.05509	0.26899	1.78141	1.21965	0.20417
043	1.54120	0.90392	-0.57187	-0.33708	0.19956	-0.40416	-0.06875
044	1.39435	1.86484	-0.25235	-0.31651	1.07357	-1.00085	0.11120
045	-0.87133	-1.06449	1.94012	0.56658	-0.07726	0.84558	0.99581
046	-0.68572	-0.29035	0.82163	0.62394	-0.68572	-0.16679	1.19229
047	1.08323	-0.44656	-0.87401	-1.16647	0.25084	-1.03149	-1.52642
048	1.74850	-0.07470	-1.16356	-1.01162	-0.42921	-0.35324	-1.39146
049	0.36746	1.41735	-1.26263	-0.76531	-0.93109	-0.57191	-0.82057
050	0.00902	-0.61476	-0.82817	-0.97591	0.50150	-0.04021	-0.71326
051	1.92374	0.18951	-1.24077	-0.82956	-0.18593	-1.22289	-0.31108
052	1.93344	-1.00419	-0.94424	-0.52457	0.22481	-0.97421	-0.67445
053	1.35832	-0.39303	-1.37054	-1.22798	0.34008	-0.92251	-0.69850
054	-1.14693	0.87104	0.56883	1.08552	-0.52301	1.16351	1.27074
055	-1.10007	0.13958	1.07664	0.93022	-0.36799	0.95951	1.21329
056	-0.93250	0.02291	1.98249	1.01732	-0.67902	1.04657	0.85158
057	-0.63219	-0.32000	1.93366	0.86049	-0.68097	0.50927	1.18244
058	-0.92001	0.11800	1.63584	0.97974	-0.53810	0.84264	1.18538
059	-0.93716	-0.60640	1.92945	1.92945	1.04742	0.27563	0.49614
060	-1.36114	1.33448	-0.14663	0.74203	-0.02814	1.06788	0.32732
061	-1.00443	-1.47878	1.81794	1.29616	0.46604	0.98783	0.65578
062	1.17334	-0.20141	-1.09661	-1.00069	0.27814	-1.09661	0.11829
063	-2.46092	0.51381	0.24338	0.24338	1.05468	0.51381	0.78425
064	1.59703	-1.40473	-0.23216	1.12800	0.75278	-1.54543	-0.65429
065	-0.73797	-0.22381	0.68353	-1.01017	-0.52625	0.62304	-0.97993
066	0.10996	0.05588	0.54260	0.74090	-1.47639	1.73237	0.81300
067	0.31410	0.13960	1.09936	0.92486	-1.32185	1.27386	1.14299
068	0.48134	-0.39810	1.37649	1.06240	-1.49741	0.63838	1.18804
069	-0.46663	0.02415	0.99039	0.99039	-0.90374	1.37382	1.29714
070	-0.79013	-0.36092	-0.26988	-0.35659	1.68107	0.03359	-0.31323
071	0.10577	-0.82206	1.33051	1.20680	-1.11896	1.26865	1.24391
072	-2.00322	0.59156	-0.18567	-0.18567	0.30094	0.39879	0.91651
073	0.62635	0.32809	0.48869	1.70469	-0.88791	0.46575	0.48869
074	0.43420	-1.14868	0.94402	-0.01804	1.03447	0.02306	-0.98423
075	0.90832	-0.40310	0.69333	0.52134	-0.38160	-0.31710	-0.38160
076	1.06321	-1.69905	1.11532	1.11532	0.07296	0.69838	0.07296
077	-0.46797	-0.34175	1.27963	1.18254	-1.42915	0.72622	1.26992
078	-2.32701	0.73202	1.95972	0.32278	-0.39337	0.07724	0.68086
079	-2.57428	-0.01598	1.26315	1.10326	0.54363	0.50366	0.26382
080	-1.94062	0.46323	0.12277	0.12277	0.51997	0.34458	1.09772
081	-2.03171	0.14893	-0.06431	-0.06431	1.29084	0.92625	-0.27068
082	-3.07033	-0.12734	2.02330	-0.12734	-0.12734	-0.12734	-0.12734
083	-2.12871	1.02343	-0.44441	0.20495	0.48905	0.44170	1.26694
084	-2.87877	-0.38505	1.05738	-0.40950	-0.21392	-0.33616	0.51952
085	-0.85691	0.85691	-1.07114	-1.07114	-0.85691	0.00000	-0.21422
086	-0.81731	0.14423	-0.81731	-0.81731	1.10577	-0.81731	-0.81731
087	-0.84325	-0.16865	-0.84325	-0.84325	-0.16865	-0.84325	-0.84325

088	-0.40944	2.32020	-0.40944	-0.40944	2.32020	-0.40944	-0.40944
089	-0.32489	-0.32489	-0.32489	-0.32489	-0.32489	-0.32489	-0.32489
090	-0.31198	-1.10366	0.57332	0.55629	0.11364	0.09661	0.14769
091	-2.34523	0.14087	0.41711	1.52205	0.96958	0.96958	0.69335
092	-0.30420	-0.30420	-0.98023	-0.30420	-0.81122	-0.30420	-0.30420
093	-0.13236	-0.24422	-0.24422	-0.24422	-0.35607	-0.24422	-0.24422
094	-0.92320	0.47030	-0.92320	-0.22644	2.21219	-0.22644	-0.22644
095	1.40677	-0.05861	-0.05861	-0.05861	1.99293	-0.05861	-0.05861
096	-0.46908	-0.43752	0.04379	0.18582	-0.53221	-0.01933	1.11689
097	-1.42959	1.02614	0.04385	0.95598	1.02614	1.76287	0.32450
098	-1.68304	0.13268	-0.14665	0.41203	0.06285	1.11039	-0.42599
099	-0.99132	0.29181	0.41598	0.37459	0.27111	0.62294	-1.38454
100	-1.65517	-0.04675	0.28988	0.51432	0.85096	1.67387	-0.08416
101	-0.25903	-0.75063	1.06450	0.34601	-0.56156	-0.48593	0.53509
102	-0.51133	0.25293	0.61687	1.01720	0.03457	0.54408	1.23556
103	-0.32201	0.06133	1.13472	0.90471	-0.51369	-0.13033	1.01971
104	1.54745	-0.24712	-0.98260	-1.15911	-0.48247	-1.18853	-0.77666
105	1.66103	-0.08389	-0.26845	-0.35234	-0.11744	-1.04024	0.31878
106	0.90105	-0.29680	-0.77594	-1.17522	-0.05723	-0.72270	-0.96227
107	1.57326	-0.03277	-1.27828	-1.24550	-0.19665	-1.21272	-0.85218
108	-1.12851	-1.12851	1.51574	1.02274	0.21602	0.03675	1.24683
109	-2.03438	0.21645	0.60293	0.60293	0.77551	0.44980	1.10123
110	0.17003	-0.05858	-0.88731	-0.88731	-0.41579	-0.88731	-0.88731
111	0.25088	0.77123	-1.16149	-1.27299	1.10574	-0.97565	-1.16149
112	-1.88636	0.27879	0.62801	0.62801	0.81426	0.48832	1.11691
113	0.38584	-0.37394	-0.95066	-0.99643	1.36534	-1.37175	-1.85692
114	-0.55996	0.37790	-0.72547	-0.72547	1.75713	-0.78064	-0.39445
115	0.11167	-0.14803	-0.82326	-0.82326	1.66990	-0.56356	-1.18685
116	-1.67420	1.35326	0.11969	0.37499	1.13923	2.16889	0.41628
117	-1.97417	1.58029	0.17746	0.25587	1.34074	0.66087	0.29379
118	-1.94151	0.53710	0.33538	0.31570	1.78938	-0.32535	-0.28016
119	-1.55208	0.00926	0.11511	0.77670	0.61792	1.67646	0.51206
120	-1.39169	0.12193	1.17306	-0.08829	-1.09738	0.12193	0.54238
121	1.90603	-0.28062	-1.32535	-0.91231	0.15670	-1.56831	-0.66935
122	0.53413	-0.50895	-0.52694	-0.92259	0.53413	-0.90461	-0.81469
123	2.26155	0.40631	-1.23427	-0.52897	-0.14565	-1.08094	-0.05366
124	-2.38450	0.19857	-0.12431	0.94121	0.61832	-1.48042	-0.67321
125	-0.07936	-1.31533	-0.63880	0.05073	-0.28752	-1.31533	-0.75589
126	3.36880	-0.00868	-0.43481	-0.57685	0.13336	-0.34011	-0.45059
127	-0.92597	0.16365	-0.99667	-0.79704	2.33873	-0.55167	-0.88438
128	0.66694	-0.17551	1.32218	1.04136	-1.62640	0.66694	0.94776
129	-1.05495	0.03169	-0.91912	-0.78329	2.34082	-0.60218	-1.05495
130	0.36375	-0.45829	1.43241	0.85698	-1.07482	0.44596	0.69257
131	0.58921	0.02129	1.15713	0.87317	-2.39234	0.73119	0.87317
132	-1.12343	-0.46685	1.47730	0.64165	0.18972	0.21530	1.23854
133	0.81945	-0.93050	0.88675	0.88675	0.28100	0.61753	-0.89685
134	1.16146	-1.31179	0.14306	1.98588	0.43403	-1.26330	-0.48737
135	-1.07351	0.53577	1.00678	-0.91651	-0.20999	0.61427	-1.03426
136	1.33050	-1.25447	0.03801	1.25447	0.79830	-1.48255	-0.57021

137	1.72407	-1.41940	-0.05837	1.00653	0.97237	-1.55038	-0.57658
138	-1.48640	0.37888	0.26230	0.76749	0.80635	1.70013	0.14572
139	-0.40510	-0.26950	1.62890	0.81529	-0.77800	0.17119	0.67969
140	-1.24491	0.26407	0.51557	1.34551	0.61616	2.02455	0.44012
141	-0.29017	-0.29017	1.86543	1.22289	-0.64253	-0.22799	0.82908
142	1.39053	-0.66570	-0.40867	-0.85848	0.76080	-1.11551	-1.33398
143	0.79522	-0.42715	-1.24207	-0.30491	1.33850	-1.64953	-0.97043
144	0.31060	-0.22716	-0.63512	0.27351	2.79545	-1.89609	0.14371
145	0.90975	1.22631	-0.39356	-0.48767	-0.93256	-0.73863	0.62741
146	0.00000	0.00000	0.00000	0.00000	2.17944	0.00000	0.00000
147	1.38593	-0.06188	-0.94925	-0.64567	1.52604	-1.50969	-0.66903
148	0.71922	0.48394	-1.34898	-0.46261	1.72049	-1.27785	-1.19578
149	0.11614	-0.27100	-1.12275	-0.81302	2.51651	-1.43247	-1.27761
150	-1.99493	0.17750	0.57624	0.57624	0.75499	0.59274	1.18123
151	0.03013	-0.90727	1.67058	1.43623	-1.14162	0.80014	1.10145
152	-0.23819	-0.88606	0.79079	1.05756	-0.35252	0.79079	1.07026
153	0.18033	-0.08882	-0.78863	-0.78863	1.79529	-0.51947	-1.16545
154	-2.20894	0.65805	-0.30799	-0.04830	0.84503	0.22177	0.87620
155	-4.03180	0.28602	0.31160	0.28237	0.42484	0.09972	0.28602
156	3.56721	0.04398	-0.04398	-0.58500	-0.35188	-0.65538	-0.66857
157	-2.07969	0.46557	-0.00106	-0.04348	1.10188	0.50799	0.72009
158	-2.00033	-0.03279	1.06028	1.06028	-0.03279	0.84166	1.16959
159	-1.07068	-0.51783	0.14558	0.14558	0.21929	0.14558	1.61984
160	-1.76464	0.71073	-0.22690	1.01078	0.74824	1.64837	0.14814
161	-0.29422	0.34626	1.82742	0.10608	-0.89469	-0.09407	1.30701
162	1.72462	-0.68182	-1.10797	-0.93250	0.02005	-1.35864	-0.90743
163	-1.59434	1.15452	-0.33771	1.15452	0.91891	1.46868	0.01570
164	-0.45558	-0.61543	1.86229	0.14386	-0.93514	-0.29572	0.82324
165	1.91754	-0.40348	-1.24013	-1.05120	0.08231	-1.21314	-0.51143
166	1.37763	-1.00882	-0.57491	-0.73763	-0.30373	0.29288	-1.33424
167	-1.01082	-0.24613	1.85676	0.63803	-0.79575	0.37517	0.51855
168	-0.26627	-0.88832	2.47988	0.68957	-0.56971	0.79577	0.50750
169	-1.24045	0.15724	1.20551	0.50666	-0.79119	0.08236	0.43178
170	-0.28247	-0.45385	1.77417	1.28540	-0.96167	0.96167	0.71411
171	-1.67628	-0.13077	0.04755	0.99863	0.73114	1.50390	0.49337
172	-0.22945	0.22441	1.13215	-0.17902	-1.13719	0.32527	0.72871
173	-0.62732	1.53219	-0.18629	-1.02272	-0.23192	0.04182	-0.27754
174	3.62803	-0.21641	-0.48422	-0.52742	0.30194	-0.70884	-0.46694
175	3.78891	-0.60799	-0.48378	-0.17326	0.42292	-0.98060	-0.42168
176	-1.41721	-0.75558	-0.83497	0.03837	0.14423	-1.68186	-0.91437
177	-1.76104	0.28674	0.02854	0.00225	0.23792	0.27078	0.99938
178	-0.23393	-0.68380	1.55269	0.89716	-0.22107	0.38303	1.46271
179	-0.45777	-0.27209	1.29905	1.04195	-0.84342	0.62774	1.59900
180	-0.57460	-0.65764	0.87021	1.28539	-0.85693	0.35539	1.68396
181	-0.46319	-0.91326	0.81199	1.29957	-1.06328	0.24941	1.86215
182	0.89445	-0.45566	-1.58077	-0.90571	1.34450	-1.01822	-1.69328
183	0.31687	-0.33873	-1.50425	-1.06718	1.91947	-0.99433	-1.72279
184	0.26597	0.26597	1.37420	1.30031	-1.58106	1.00479	1.59584
185	-0.56475	-0.22541	1.48097	1.24828	-1.36947	1.52945	1.67488

186	-1.21487	1.11278	-0.31647	0.86776	0.86776	0.86776	0.86776
187	-0.38343	-0.48389	1.75976	0.82211	-0.68481	0.92257	1.19047
188	1.30106	-0.73778	-0.59956	-1.18702	-0.46133	-1.22158	-1.35981
189	0.90948	-1.34579	0.22909	1.98003	0.48126	-1.18878	-0.55597
190	1.10713	-1.34714	-0.03186	1.16137	1.10713	-1.59121	-0.81831
191	0.20124	-0.82250	1.25546	3.15672	-0.54828	0.09155	0.46023
192	-0.47862	-0.03907	1.28934	1.66052	-0.93770	1.87541	1.23073
193	0.08138	-0.74930	1.06081	3.23295	-0.67914	0.28063	0.44340
194	-0.52594	-0.02750	1.01236	1.74285	-0.99002	2.07801	1.10690
195	0.52353	-0.95456	1.70187	2.63215	-0.11387	-0.45497	0.46151
196	-0.24762	-0.06334	1.92914	1.06534	-0.57010	0.88107	1.37631
197	1.35506	-1.20377	0.56772	2.29291	-0.57853	-0.71747	0.52527
198	0.84030	-0.44509	0.66763	0.91704	-1.51945	0.82111	2.41347
199	0.84675	-0.85922	1.29293	2.45431	-0.86578	-0.19214	1.00641
200	-0.02304	-0.74130	1.51909	3.19951	-0.73938	0.41674	0.53005
201	3.09494	-0.96550	0.78995	0.42359	-0.72126	0.75942	0.22515
202	0.72258	-0.92193	-0.60907	1.38039	0.50197	-1.14654	-0.90989
203	0.92064	-0.96568	-1.08421	1.02563	0.37540	-0.41028	-0.70153
204	0.70607	-1.18053	-0.30625	1.59058	0.12833	-1.73782	-0.75617
205	1.01120	-0.97155	-0.32836	2.36045	0.63399	-1.52285	-0.61852
206	0.51343	-0.78445	1.67565	2.82479	-0.79099	-0.51474	0.24045
207	0.59949	-1.31907	-0.22535	1.46992	1.52916	-1.15957	-0.64461
208	1.92089	-1.74080	-0.03001	1.81884	-0.04201	-1.43466	-0.38417
209	0.23543	-0.91205	1.75737	2.34320	-0.88991	-0.21550	1.20577
210	-0.17569	0.03168	1.27592	1.09159	-1.30472	0.66532	0.45795
211	-0.58242	0.21579	1.39935	1.24246	-1.28705	0.82959	1.31402
212	-0.75415	-0.28280	0.94269	0.94269	-0.75415	0.47134	1.60258
213	-0.72880	-0.00881	-0.99565	-1.07117	1.90948	-1.05607	-0.55761
214	-1.29890	-0.11772	0.08839	-0.91046	1.00004	-0.81533	0.51647
215	0.12415	0.08484	-1.36963	-0.63584	1.65725	-0.69481	-1.15343
216	0.67057	-0.57945	-0.33567	3.59792	0.07129	-0.34772	-0.95026
217	0.65824	-0.68963	-0.15845	3.87512	-0.18946	-0.34209	-0.75709
218	-1.00880	-1.19456	1.54893	0.85591	0.72731	0.15575	0.82019
219	0.68333	0.16858	-0.22391	-0.30113	-0.25609	-0.19818	-0.13383
220	0.56496	-0.93493	2.59559	0.40343	-1.24260	0.18806	0.47266
221	0.17959	0.87840	-1.32765	-0.78528	-1.19608	-0.46365	-0.70925
222	1.66401	-0.05059	-0.92629	-0.50684	2.23064	-0.89685	-0.09106
223	-1.56377	1.31308	-0.57742	1.18978	0.90210	1.27198	0.32672
224	-1.54449	0.21103	0.02427	0.80866	0.47250	1.74246	0.36044
225	-0.29527	-0.66436	1.87826	0.07381	-0.99244	-0.21325	0.48391
226	-0.50013	-0.41607	1.62928	0.64863	-0.72428	-0.19192	1.12494
227	2.17122	-1.15456	-1.10048	-1.26271	-0.01892	-1.18159	-0.20819
228	1.49721	-0.13143	-1.24577	-1.27434	-0.16000	-0.84575	-0.81718
229	-1.42763	0.10842	-0.25299	0.28914	0.01807	0.92163	-0.43371
230	-1.70678	0.38182	-0.49930	1.29558	0.28392	-0.30350	0.08811
231	-1.65918	-0.31624	-0.14295	0.85341	0.76677	1.84979	-0.44620
232	-0.64074	0.01543	0.40142	-0.06175	-0.13895	1.44359	1.09620
233	-0.32275	0.72578	2.06921	-0.32275	-1.01085	0.85684	1.70878
234	-0.37473	0.61720	1.38870	0.17634	-0.63189	-0.66863	0.83763

235	1.99861	-0.86076	-0.61263	-1.12071	0.27353	-0.08093	1.47872
236	1.81039	-0.02948	-1.53913	-0.59560	-0.61919	-2.17601	-1.06736
237	1.74142	0.35352	-1.53192	-0.45826	0.85107	-0.48445	-1.50573
238	1.59135	-1.36818	-0.39783	-1.10133	-0.22803	-1.10133	0.01455
239	0.74534	0.17686	-1.41804	-1.60753	0.74534	-0.81798	-1.60753
240	-0.93913	-0.31202	1.40105	1.56930	-1.03090	1.21750	1.53871
241	-0.36043	0.20242	1.51125	1.05689	-1.18099	1.21287	0.60253
242	-0.36934	-0.02517	1.33875	0.94359	-1.38273	1.23677	0.70140
243	-0.38435	-0.32782	1.11349	0.83087	-1.59958	1.39610	0.94392
244	2.01761	-0.88947	1.45469	0.97661	-0.60416	0.50623	1.03058
245	-0.07884	0.82117	-0.14038	1.69811	-0.77117	1.49811	-0.07884
246	-0.62388	0.16521	0.78522	0.86977	-1.34252	2.22956	1.01068
247	-0.39892	-0.16204	2.05598	1.08155	-1.12031	0.72085	1.46917
248	-9.47725	-0.38413	1.44050	1.29112	-1.36581	0.24542	0.49084
249	1.18102	-1.62557	-0.33494	-0.66272	1.97998	-0.29397	-2.03529
250	2.27994	0.32423	-0.31908	-0.21615	-1.39987	-1.50280	-0.21615
251	0.91911	0.28437	0.03382	-0.15826	-1.27740	-1.93720	0.14239
252	-0.48513	0.33522	-0.91483	-0.85135	1.51691	-0.97343	-1.03691
253	-1.76464	0.71073	-0.22690	1.01078	0.74824	1.64837	0.14814
254	-0.29422	0.34626	1.82742	0.10608	-0.89469	-0.09407	1.30701
255	1.71967	-0.65143	-1.10069	-0.90102	0.02246	-1.40020	-0.92598
256	-1.20901	-0.24180	0.72540	1.30573	0.33852	0.91885	0.72540
257	-1.06835	-0.64101	2.09398	0.38460	-0.72648	0.29914	1.32476
258	0.11843	-0.23248	-0.32022	0.73255	2.57492	0.29390	0.73255
259	-1.98079	0.75736	0.00000	0.05825	0.87387	0.17477	0.87387
260	-0.32888	-0.82399	-0.78862	1.43933	-0.61180	0.44912	-0.11670
261	-2.37814	-0.91302	0.01608	1.69561	-0.66287	0.98091	0.87371
262	-1.96225	-0.35317	-0.18954	1.69225	0.11045	1.09226	0.19227
263	-2.29756	-0.02160	0.15125	0.81387	-0.07922	1.47649	0.66982
264	-1.43220	0.08141	0.19608	1.29689	0.56302	1.13636	0.26488
265	-0.78864	0.53483	-0.55296	1.07872	0.46231	1.47758	0.91555
266	-0.80863	0.79284	0.07105	1.19885	0.90562	1.49208	0.40939
267	-0.76624	1.13150	-0.21528	1.23353	1.04988	1.27435	0.29486
268	-0.42090	0.90158	0.74898	1.74085	0.67268	1.51195	-0.19201
269	-1.17805	0.87335	-0.06184	1.89906	1.26553	0.66218	0.17949
270	-0.31733	1.33281	0.06346	1.29049	2.00979	0.57120	0.10577
271	1.05916	1.10070	-1.64066	-0.85148	0.22844	-1.64066	-0.64380
272	0.44318	0.79616	-1.12560	-1.04716	0.24708	-2.30219	-0.53731
273	1.42573	-0.42244	-7.32817	-1.79537	-0.05280	-1.58415	-1.26732
274	1.83616	0.01276	0.74212	-1.92004	0.30450	1.03387	0.45038
275	1.06552	-0.93777	1.64619	0.25259	-0.85067	0.83325	0.68809
276	-0.81766	-0.61440	1.76929	0.60516	-0.83614	0.80842	0.67907
277	-1.03554	-0.13855	1.87968	0.48613	-0.82731	0.63029	0.88658
278	-0.89360	0.08672	1.93425	0.63344	-0.87475	0.06786	0.53917
279	0.45547	0.13301	1.34223	0.93915	-1.29117	-0.18944	0.61670
280	0.72554	0.76455	0.25745	-0.05461	-0.87377	-0.40568	-0.09361
281	2.02261	0.05778	-0.67420	-1.40620	-1.40620	-0.78978	0.13484
282	1.75741	-0.28710	-1.98361	-1.02660	-1.59211	-0.50460	-0.02610
283	0.59036	0.65559	-0.61645	-1.46448	-1.36663	-1.66018	-1.04046

284	-1.03255	-0.65901	1.10192	-0.07203	-2.52668	1.04856	0.19477
285	1.03339	-1.01163	-0.44599	1.29446	-1.05514	1.77308	0.11965
286	-0.85765	0.88672	1.21899	-0.40079	1.38512	-0.02699	1.05286
287	1.01033	1.01033	-1.07156	-0.58170	0.31636	-1.84718	-0.94910
288	0.18796	0.98321	-1.33023	-1.35433	0.30845	-1.16154	-0.72777
289	1.84092	0.29270	-1.19099	-0.86844	0.72814	-1.22324	-0.75555
290	1.59517	0.08322	-1.46684	-0.85698	0.13404	-1.07297	-0.47581
291	1.20071	-0.24313	-0.84247	-1.04679	0.27446	-0.92420	-0.78798
292	0.68417	-0.56316	-0.93550	-1.47539	-0.24667	-1.02858	-0.45146
293	0.46413	-1.16033	-0.06961	-1.74049	-0.85864	-0.99788	-0.32489
294	-0.35465	-0.64565	-0.17278	-0.57290	0.30009	-1.51865	0.48196
295	0.30495	-0.85065	1.20375	-1.30005	-0.62595	-0.75435	-0.20865
296	-0.29102	-2.02911	0.15359	0.75990	-1.30154	0.43654	1.16411
297	0.85975	-0.50885	-1.70253	-1.09540	1.11701	-1.31150	-1.63050
298	0.54314	-0.41769	-1.54534	-1.17168	1.72417	-1.28512	-1.67212
299	0.08650	-0.64146	-0.91563	-0.97236	2.23260	-1.07635	-1.04799
300	0.64294	0.76134	-1.41731	-0.56479	-0.92001	-0.23325	-0.99105
301	-1.68323	-0.42651	-0.04569	0.41128	0.63977	1.17292	-0.38843
302	0.34083	-1.08185	0.94307	-1.08185	1.41439	-1.08185	-1.08185
303	-0.19808	-0.37981	0.03816	-0.59789	-0.70693	-1.50655	-0.30712
304	-1.39466	1.67542	0.99318	-0.37129	-1.05353	1.25558	0.75702
305	2.71965	0.19508	-1.06720	-0.33565	-0.69425	0.99835	0.00860
306	0.88050	1.98619	0.09843	-0.89938	-0.49486	-1.66796	0.04449
307	-1.89101	0.55974	0.10589	0.74127	0.83204	0.98332	0.65050
308	3.15795	-0.57590	-0.57590	-0.57590	-0.57590	-0.57590	0.63803
309	2.16386	-1.34414	-0.58613	-0.18068	-0.39222	0.29527	-1.32652
310	-1.15917	-0.26290	1.70888	-0.41228	-0.50191	0.42423	1.02174
311	0.53426	-0.27486	-0.86981	0.20109	-0.63183	-0.41765	0.17729
312	2.53344	0.24884	-0.72289	-1.59762	-0.75321	-0.12408	-0.78353
313	1.63522	0.03840	-0.21985	-0.87704	-0.90231	-0.18358	-0.29348
314	0.49625	-0.56891	1.25328	1.25328	-0.73820	0.76445	0.88428
315	-0.59601	0.33220	1.39720	1.12362	-0.51784	0.69371	1.44605
316	2.04437	-1.15448	0.13230	0.19120	-0.41141	-0.34797	-0.30719
317	0.67357	-0.87609	1.13255	1.19880	-0.88082	0.69486	0.66174
318	1.27450	-1.16122	0.86646	0.93983	-0.87129	0.34567	0.33672
319	-1.68456	0.35792	0.26899	0.14086	0.76642	0.50112	0.96841
320	0.47877	-0.31258	1.24374	0.76893	-1.77659	0.61066	0.92720
321	-0.64734	0.37747	1.31120	1.19733	-1.52414	1.26565	1.26565
322	1.41178	0.49355	-0.19512	-0.19512	0.03443	-1.57247	0.49355
323	1.41178	0.49355	-0.19512	-0.19512	0.03443	-1.57247	0.49355
324	0.96764	0.18002	-0.83262	-0.83262	-0.27003	-0.15752	-0.83262
325	-1.11857	-0.49714	-0.18642	-0.18642	-0.65250	-1.11857	-0.80786
326	-0.17534	-0.52602	-0.52602	-1.22738	0.00000	0.00000	-0.17534
327	-0.55892	-0.41742	-0.84192	-0.55892	-0.27592	0.00707	-0.55892
328	-0.85754	0.49002	0.00000	1.83760	-0.36752	0.73504	0.98005
329	-0.97267	-0.30948	-0.30948	0.13263	1.90113	1.45900	-0.08842
330	-1.49545	-0.13595	0.40785	0.40785	0.13595	1.22355	0.67975
331	-0.83146	1.86900	0.30557	0.16344	0.44770	2.29540	1.15835
332	-0.76295	0.97385	0.60167	0.35356	-0.14266	2.09036	2.21442

333	-1.45063	0.19781	0.69234	1.51657	2.01111	0.03296	1.35172
334	-1.31643	1.25221	-0.99535	-0.35318	1.41275	0.44951	-1.15589
335	-1.09206	2.90177	-0.46802	-0.46802	1.15447	-0.09360	-0.46802
336	3.73347	0.51922	-0.22252	-0.22252	0.51922	-0.09889	-0.46977
337	0.56459	0.56459	0.31366	-0.18819	0.56459	-0.43912	-2.19564
338	-0.72442	-0.07325	-0.56163	-0.88721	0.41511	-1.70117	0.25232
339	-1.95409	0.29886	0.16092	0.75864	0.55174	1.24142	0.39081
340	-1.03769	-0.50949	-0.77359	-0.35543	-0.79560	-0.66355	-0.13535
341	-0.86872	0.00603	0.63947	0.98636	0.23226	1.24275	0.57914
342	-1.13447	0.96175	0.01697	0.10554	1.16843	0.60746	0.32698
343	-1.16886	-0.70513	1.80444	0.60420	-0.92336	0.60420	0.68604
344	-0.85682	-0.65173	1.78656	0.87505	-0.62894	0.87505	0.71553
345	-1.21925	0.10567	-0.17823	-1.31389	-1.12461	-0.80915	0.07413
346	1.48550	-0.07681	-1.19647	-1.45686	0.26168	-1.24855	-0.46739
347	-0.48154	0.95284	-0.24248	-0.85722	-0.48154	-1.54026	0.20149
348	1.37989	-0.53694	-1.55309	-1.36834	0.71015	-1.04502	-0.79098
349	1.71580	-0.26966	-0.18076	-0.86234	0.35264	-0.50674	0.44154
350	1.66062	0.64012	-0.87515	-0.47313	-0.10204	-1.12254	-1.12254
351	1.41819	-0.20903	-1.11027	-1.33558	0.26661	-1.31055	-0.58455
352	-0.28584	0.22232	2.06440	0.79400	-1.04808	0.66696	1.30216
353	-1.68149	0.53599	0.58850	0.73411	-0.42595	0.94416	1.45020
354	-0.14308	0.37722	1.24441	0.98425	-1.87746	0.98425	1.24441
355	-0.45632	0.36302	-1.10408	-1.10408	0.85849	-0.73516	-1.15127
356	0.10514	0.60673	-1.28456	-1.28456	1.23716	-0.66333	-1.38580
357	-1.86253	1.19080	-0.64120	-0.03053	-0.64120	-0.94653	0.27480
358	-1.16469	-0.17499	1.50749	1.07562	0.18489	0.00494	1.21957
359	-1.68570	-0.43806	1.44726	1.66906	0.19962	0.89275	0.36597
360	1.61767	-0.33495	0.65443	0.56726	-0.32187	-0.39597	-0.04293
361	-0.33550	1.37797	-0.01286	-0.05210	0.19641	-0.19598	1.89245
362	-0.09913	0.21897	-1.37159	-1.17549	-1.64177	0.31048	0.29741
363	-1.96860	-0.48556	1.17497	1.17497	0.02404	1.51853	0.86577
364	-0.89264	-0.89264	1.11704	0.31170	-0.85970	1.08043	-0.23739
365	-0.67069	-0.64068	1.24985	1.21985	-0.67069	1.01979	1.92005
366	-1.74040	0.66015	0.38580	0.96879	0.79732	0.69444	0.52297
367	-1.13076	1.72997	0.32966	0.18567	0.20308	-1.70038	-0.17666
368	-1.19114	-0.64525	1.30661	0.32478	-1.15187	0.25016	0.09307
369	0.07836	-0.60617	-0.61973	-0.63329	0.15461	-0.23340	-1.00267
370	1.67582	0.94075	-1.03057	-0.66696	-0.12450	-1.12098	0.69310
371	-0.28847	0.22362	-2.30071	-0.54731	0.69398	-0.33022	-0.56122
372	2.84390	0.11022	-0.57276	-0.79672	0.30426	-0.79672	-0.46078
373	-0.59755	0.19580	1.18073	-0.69446	-0.22003	-0.05437	0.34455
374	3.45534	-0.92229	-0.56825	-0.36492	0.08719	0.28095	-0.69025
375	1.34494	0.34014	-1.96717	-1.20054	0.21361	-1.18938	-0.39670
376	-1.50357	0.64171	0.01808	0.54193	-0.01933	0.84127	-1.05455
377	-0.08831	-0.45824	-1.37842	0.97058	0.69314	0.10126	-1.53564
378	-1.21413	-0.27270	1.50781	-1.04017	-0.65132	-0.45178	2.02457
379	-1.09363	-0.61745	-1.21764	-1.21764	-0.29561	0.82673	1.13342
380	-0.63807	-0.63807	1.48884	1.48884	-0.63807	-0.63807	1.48884
381	-0.46012	0.45571	-1.13873	-1.10438	0.67802	-0.52558	-1.37595

382	0.40209	0.07465	0.88015	0.92599	-1.94890	1.16174	0.39554
383	0.71061	0.22793	-0.14748	-0.30837	0.97876	-0.25474	-1.43462
384	-0.80756	0.65158	1.10442	1.00379	-1.31072	0.95348	1.50695
385	0.14238	0.08865	0.06179	-0.60985	0.24985	-1.55015	-0.09940
386	0.74519	-0.99312	-0.22370	-0.10971	-0.73665	0.03277	3.08196
387	1.48482	-0.74314	0.86920	0.19494	-0.62588	0.78125	1.86592
388	0.17263	0.37572	-1.04594	-1.04594	1.06625	-0.88346	-1.00532
389	1.22234	-0.89663	1.18217	1.20393	-0.77110	0.57460	0.69511
390	0.74230	0.80228	-1.48044	-1.39713	0.94558	-0.83061	-1.64040
391	-2.51433	0.81528	-0.78855	-0.48373	0.66053	-0.12732	0.60894
392	0.16811	0.62509	-0.58221	-0.55400	-1.77259	-0.23243	0.25274
393	-0.65858	0.20419	2.13106	1.61340	-0.42851	1.12449	0.52054
394	-0.40733	0.76244	1.09667	2.01578	0.05222	0.42822	0.38644
395	0.29169	0.35360	0.38579	0.38083	0.22236	0.25950	0.05893
396	0.28445	0.30140	0.43945	0.39102	0.23359	0.26508	0.13429
397	-0.50967	0.81778	0.21693	0.10514	0.38461	0.07021	0.82477
398	-1.12700	-0.16825	1.72046	1.19315	0.31111	0.11936	1.41366
399	-2.58326	-0.36209	1.30215	1.30215	0.07393	0.19049	0.95678
400	-0.62033	1.73431	-0.61439	-0.61439	1.63849	-0.55507	-0.60436
401	-0.03193	0.88373	-0.00367	-0.02628	2.09898	-0.16193	-0.30889
402	-0.79025	-0.32853	1.25198	1.34077	-1.16318	0.86129	1.55387
403	0.96709	0.80898	0.38736	-0.24506	0.17655	-0.61398	0.33466
404	1.33680	0.09567	-0.57661	-0.99032	0.35424	0.66452	0.66452
405	1.28572	2.11209	-0.22117	-0.17256	-0.12395	-0.02673	-0.22117
406	0.57187	-0.07962	-0.65874	0.10134	-1.16546	0.13753	-0.36918
407	0.10406	-0.43419	-0.61360	-0.57772	-0.39830	0.10406	0.03229
408	-1.10087	-0.43798	0.10653	-0.41430	0.15388	-0.27225	-0.27225
409	-0.91059	0.84150	-0.93527	-0.26898	-0.54043	0.19988	-0.04688
410	-0.99035	-0.77412	0.35030	1.08549	-0.42814	1.43147	0.17731
411	-1.31211	-0.28764	0.85504	0.63832	0.46101	2.15533	0.69742
412	-1.34694	-1.05926	0.23527	1.01611	0.54350	1.36543	-0.03184
413	-1.64353	-0.36817	0.64249	0.66655	0.28154	0.37779	0.37779
414	-1.63362	-0.16445	0.01096	0.80036	0.29602	1.76519	-0.38373
415	-1.33669	-0.50948	0.22372	1.44574	0.35532	2.21655	0.59972
416	-1.59494	-0.00774	1.07619	1.17298	1.32782	1.42460	0.37937
417	-1.17997	-0.15470	-0.13639	1.23673	1.20011	0.68748	-0.55749
418	-0.63680	1.29869	-0.94743	0.84468	1.05974	0.82079	0.46236
419	3.46002	1.34183	-0.62088	-0.58201	0.44792	-0.42655	0.15643
420	0.33488	2.03589	0.65382	0.76013	1.34485	0.49435	0.17541
421	-0.04895	-0.31600	-0.04895	-0.34567	0.42579	-0.07863	-0.43469
422	0.28843	0.46927	0.22815	-0.40477	0.37885	-0.52533	-0.07323
423	-0.47812	-0.26718	0.01406	0.71718	0.71718	0.57655	0.08437
424	0.20523	0.12802	-0.09071	-0.59253	-0.63114	-0.43813	-0.32232
425	0.61786	-0.62245	-0.97464	-0.85214	1.70505	-0.59182	-1.15839
426	1.20933	-0.28869	-0.84137	-0.94317	0.99117	-0.43413	-0.75410
427	0.57884	-0.78157	-0.51482	-0.38145	0.87227	-0.88827	-1.66184
428	-0.75756	-1.14605	-1.20155	-0.81306	2.01738	0.46341	-1.31255
429	1.13748	0.13627	-0.52007	-0.72031	-0.38379	-0.85936	-0.13071
430	1.54872	0.30073	-0.30226	-0.82130	-0.65338	-0.83657	0.04885

431	0.77610	-0.06846	-1.44621	-0.56752	0.44339	-0.46941	-1.01113
432	1.15416	-0.30217	-0.77692	-0.21235	-0.05196	-0.29148	-0.59942
433	0.98642	-0.24755	-0.59795	-0.12568	-0.11044	-0.44560	-0.52177
434	0.04815	-0.14689	0.38949	0.74302	-0.52480	0.34072	1.43789
435	3.38103	-0.32641	-1.13238	-0.48761	0.07656	-0.32641	-1.05178
436	0.51381	1.05468	-0.74819	-1.10876	1.05468	-0.92848	-1.10876
437	-0.63503	0.14339	0.51212	0.62137	0.36190	0.53943	0.17070
438	0.65764	-0.64336	-0.81789	-0.96069	1.29229	-0.86549	-0.88136
439	0.38723	-0.68050	-0.58084	-0.09680	1.41225	-0.48119	-0.46695
440	1.74962	-1.11665	0.79419	0.95343	0.43591	-1.07684	-0.67875
441	1.77412	-1.16263	0.40631	1.09022	0.60746	-1.04194	-0.63965
442	-0.27486	-0.91622	0.64135	1.25217	0.82460	-0.51919	-5.42514
443	-0.12983	-0.54656	0.47924	1.79358	0.79981	-0.64273	-0.16188
444	-1.46579	0.21060	0.95724	0.92906	0.01338	0.21060	1.77431
445	-1.03884	0.82734	0.57851	0.95175	-0.36701	-0.36701	0.70293
446	-0.02248	-0.68633	1.24097	1.11248	-0.16167	0.93046	1.08036
447	-0.04786	-0.46672	1.13888	1.10897	-1.96264	0.80978	1.15883
448	-0.27098	-0.45200	1.02804	1.01740	-1.65520	0.74055	1.28359
449	-0.39289	-0.42563	1.00406	0.98223	-1.50609	0.74213	1.28781
450	-0.60309	-0.63857	0.93420	0.94603	-0.37841	0.79230	1.27714
451	-0.83093	-0.86545	0.66520	0.65369	-0.72735	0.66520	1.05650
452	-0.95890	-0.99172	-0.18784	-0.12222	0.52580	0.09105	0.56681
453	-0.16997	-0.07554	-0.35883	-0.42178	-0.07554	-0.35883	-0.42178
454	3.17131	-0.48009	-0.88580	-1.21037	-0.66942	-0.42599	-0.20961
455	0.66774	1.36872	-1.18139	-0.06949	0.09970	-1.10888	-1.06053
456	1.33341	-1.38103	-0.19048	1.80963	0.61908	-1.19054	-0.61908
457	0.90130	-1.38168	0.04518	2.09037	0.37812	-1.38168	-0.47800
458	0.83812	-1.24675	0.71302	2.50602	-0.24601	-0.91317	0.25435
459	0.99426	-1.37302	0.09469	1.70444	0.80487	-1.23099	-0.52080
460	0.51655	-1.13957	-0.50866	0.95030	1.14746	-1.06071	-0.90298
461	0.81331	-0.80565	-0.42006	0.01495	1.97255	-0.81307	-0.66229
462	0.90969	-0.67868	-0.70335	-0.17595	1.60364	-0.96551	-0.95009
463	1.29254	-1.03109	-0.95178	-0.66389	1.37185	-1.29254	-1.12216
464	0.25468	-0.85837	-0.83007	-0.15092	2.41477	-0.99043	-1.04388
465	0.51591	-0.85546	1.39359	2.25208	-0.44131	-0.70187	0.07432
466	0.71942	-0.81163	1.37476	2.25917	-0.71304	-0.55065	-0.00840
467	1.35830	-1.05614	0.95823	1.63554	-1.05263	-0.89471	0.14406
468	0.16757	-0.81625	1.06761	3.09742	-0.84057	-0.62975	0.62705
469	0.89952	-1.13022	0.69690	1.58202	0.99905	-1.03069	-0.38728
470	1.10366	-1.03761	0.64012	1.64103	0.41451	-1.00890	-0.57818
471	1.72673	-1.35776	0.02059	0.64673	0.18868	-1.42080	-0.62656
472	0.32728	-1.30120	0.21388	2.33681	1.17555	-1.25130	-0.29870
473	-1.96559	0.16353	1.60409	0.16353	-0.38007	0.53500	1.02424
474	-3.46804	0.03868	1.14997	0.34326	-0.16710	0.95241	0.63137
475	-2.82412	0.22273	1.15780	-0.75436	-0.32359	0.03362	0.72704
476	-1.59296	0.36782	1.34106	-1.24946	-0.06154	-0.09016	0.88307
477	-3.04677	0.13518	1.11124	-0.22595	-0.35284	-0.15763	0.67201
478	-2.77183	-0.45979	0.94488	-0.20677	-0.80878	-0.15442	0.48247
479	-2.74633	-0.17211	1.02062	0.25817	-0.08907	-0.16456	0.31856

480	-1.34469	-0.10444	2.13671	-0.24224	-0.63390	-0.56137	0.23644
481	-0.80110	-0.27228	1.42668	0.04275	-1.02613	0.09901	0.94287
482	0.50854	1.02135	0.67948	0.76495	-0.26068	-0.26068	1.02135
483	-0.55940	0.17532	-0.55940	-0.55940	1.30020	-0.55940	-0.55940
484	-1.95095	0.34515	0.47992	0.48237	0.53138	0.54854	1.16116
485	-1.95429	0.36033	0.45525	0.45769	0.53801	0.53070	1.13674
486	-1.09359	-0.61639	-1.21787	-1.21787	-0.29576	0.82765	1.13336
487	-0.43265	-0.26783	1.91977	1.05821	-1.32417	0.63118	0.83346
488	-0.30364	-1.70598	1.56803	1.57948	-1.35110	-0.30364	2.32358
489	-0.65022	-0.52781	1.00070	1.65450	-1.13684	-1.23834	2.42175
490	-1.07624	1.85306	0.50532	-0.20589	-1.24187	0.90802	-0.91711
491	-0.86397	-1.63708	2.45163	-0.00717	0.18012	-0.19447	0.58262
492	-0.64409	0.26763	-1.26171	-0.99701	0.59115	-0.70291	-1.26171
493	-0.75441	-1.30225	1.36844	1.57388	-1.30225	0.84343	1.57388
494	-0.02826	-0.87448	1.67079	1.43940	-1.17528	0.81134	1.10884
#	P	S	T	W	Y	V	
001	0.08779	0.32193	-0.26339	1.10236	0.71215	-1.82427	
002	1.15323	-1.14717	-1.14717	2.00074	1.06847	0.39046	
003	-0.23542	0.00226	-0.14487	-0.22410	-0.65421	0.12676	
004	-0.31028	-0.25084	-0.13196	0.07014	-0.40539	0.14147	
005	-1.83270	-0.77607	-0.44815	0.60847	-0.44815	0.93638	
006	-1.24687	-1.24687	0.53437	0.15267	0.53437	1.48862	
007	1.16478	0.55421	0.13150	1.16478	0.55421	-1.65324	
008	0.99075	0.96664	0.20731	-1.46805	-0.08196	-0.49176	
009	-0.53499	-1.29928	-0.63308	1.99081	1.20609	-0.06498	
010	-0.41592	-0.88802	-0.58588	1.14201	0.27334	0.93429	
011	-0.40800	-0.63921	-0.58141	1.50917	0.15077	1.06600	
012	0.30783	-0.78987	-0.20522	1.64418	0.40329	0.11693	
013	0.39536	-0.77276	-0.18228	1.96144	0.16430	-0.05391	
014	-0.10093	0.53258	0.39299	-1.20691	-1.45388	-0.72371	
015	0.47417	-1.22511	-0.46293	0.63661	0.63661	1.06143	
016	-4.23717	0.24106	0.16411	0.08822	0.13578	0.27099	
017	0.05986	0.18864	-0.53636	1.16169	0.69425	-1.30908	
018	-2.21981	0.20927	0.35875	-2.21981	0.32138	0.39612	
019	-0.98342	-1.05026	-0.44868	1.13882	-1.37612	0.44533	
020	0.00569	0.16515	0.55242	-1.23582	1.01941	1.77116	
021	-1.37833	-0.58538	-0.72531	0.20756	0.20756	0.48743	
022	-0.45855	-1.16559	-0.69423	2.39011	1.25269	-0.36633	
023	-1.76611	-0.75068	-0.44061	0.50617	2.46485	-0.20332	
024	1.99782	1.11570	0.26626	-0.77919	0.23359	-1.20391	
025	-0.39960	0.84829	0.52107	0.47670	0.12174	2.44561	
026	-1.77951	0.00000	1.77951	0.00000	0.00000	1.77951	
027	-1.22540	-1.22540	-1.22540	0.52517	0.52517	-1.22540	
028	-0.86438	-0.86438	-0.86438	1.86525	0.95537	-0.86438	
029	-1.41305	-0.81175	-0.81175	1.59344	1.59344	-0.81175	
030	-0.48733	-0.48733	-0.48733	-0.48733	-0.48733	-0.48733	
031	-0.97467	-0.97467	-0.97467	0.97467	0.97467	-0.97467	
032	-0.53052	-1.24198	-0.70014	2.02081	1.21984	-0.23840	
033	-0.57788	-1.26448	-0.69231	1.93963	1.36747	-0.34902	

034	0.26400	0.00643	0.13522	-0.50869	0.69327	-1.10967	
035	-0.53081	-0.30250	-0.24543	-0.01712	-0.70204	1.52395	
036	-0.64699	-0.11883	-0.11883	-0.64699	-0.77903	1.20155	
037	1.44000	1.19478	-0.08582	-0.08582	0.40461	-1.33919	
038	-1.52976	-0.81824	-0.60479	0.28460	-1.10285	0.21345	
039	-1.29926	-0.75620	0.43851	0.92726	1.19879	1.82331	
040	1.54899	1.19478	-0.03133	-1.06672	0.40461	-1.09397	
041	1.77345	-0.47770	0.12496	0.81626	-0.58406	-0.70814	
042	-2.17248	-0.09830	-0.55203	-1.30824	-0.59524	0.52826	
043	0.50143	2.01078	0.46789	-1.10852	0.13248	-0.67249	
044	1.26604	-0.12403	-0.27373	-1.77074	-0.05988	-1.42857	
045	-0.80695	-0.87133	0.28758	0.97435	0.07296	1.40358	
046	-1.52589	-0.56217	-0.66101	0.42626	2.32899	1.90890	
047	1.35320	0.97074	0.25084	-1.12148	0.56580	-1.25646	
048	1.77383	1.26738	0.43174	1.52060	0.05191	-1.01162	
049	0.36746	0.86478	-0.07459	-0.32325	-0.18511	-0.73768	
050	3.55483	0.89547	0.38659	-1.17290	-0.31928	-0.59835	
051	-0.86532	0.76163	-0.31108	-0.32896	0.56496	-0.97259	
052	-0.58453	0.55455	-0.25479	2.38308	1.12409	-1.03417	
053	2.19327	1.13431	0.03461	-0.98361	0.23826	-1.08543	
054	-0.28904	-1.12744	-0.85447	1.17325	1.28049	1.05627	
055	-0.28990	-1.18791	-0.85604	1.91609	1.21329	0.78381	
056	-0.19157	-0.71802	-1.30297	1.14406	0.89058	1.04657	
057	-0.28097	-0.88585	-0.68097	1.39707	0.56780	1.10439	
058	-0.22473	-1.08648	-0.89063	1.53792	0.95036	0.96995	
059	0.38589	-0.49614	-0.27563	0.16538	-0.16538	1.48843	
060	-1.62774	-0.62058	-0.29474	0.86052	-1.62774	-0.23549	
061	-1.47878	-0.79097	0.39489	-0.34034	1.01155	1.48590	
062	1.46108	0.78968	0.11829	0.69377	1.07742	-1.70406	
063	0.24338	-1.10876	-0.02704	1.05468	1.05468	-0.02704	
064	0.09615	0.94039	0.51827	-1.73304	-0.74809	0.75278	
065	-0.52625	1.40940	0.71377	-1.67555	-0.97993	0.01814	
066	-1.26007	-0.01622	0.25417	-0.10635	0.23615	1.10143	
067	-0.86378	0.09597	0.16141	0.27047	-0.10033	0.85942	
068	0.12013	-0.17824	-0.05260	0.81113	0.26147	1.07811	
069	0.45359	-0.45896	-0.06786	1.52720	0.76034	0.68365	
070	-0.71209	-0.47364	-0.13981	-0.09646	-0.00975	-0.58203	
071	0.37793	-0.72309	0.21711	0.93463	-1.04474	1.14494	
072	-0.70534	-1.03062	-0.57607	2.18167	1.43489	-0.63990	
073	-0.93379	-0.79613	-0.22255	0.44280	1.86529	0.69518	
074	-3.10983	0.12585	-0.71699	-0.95134	0.02306	0.66567	
075	2.75722	-0.31710	-0.55359	0.17736	-0.53209	0.56434	
076	-1.02151	0.22931	-0.29186	1.48015	0.28143	0.90685	
077	0.23107	-0.50680	-0.21553	1.71653	0.46408	0.71651	
078	0.40463	-0.98676	0.77294	0.95709	0.68086	1.42772	
079	-2.57428	-0.37575	-0.05596	0.78347	0.26382	0.98334	
080	-0.53751	-1.11526	-0.59941	2.22743	1.39691	-0.39307	
081	-0.62151	-0.71782	-0.62151	1.83428	-0.19502	-0.62151	
082	-0.12734	-0.12734	1.06117	-0.12734	-0.12734	2.02330	

083	0.11025	-0.97878	-0.66086	1.18577	1.74044	-0.66086	
084	1.47300	0.32393	1.20407	0.34838	0.51952	1.32631	
085	-0.85691	1.49959	0.00000	-0.85691	-0.21422	-0.64268	
086	-0.81731	0.14423	0.14423	0.14423	0.14423	-0.81731	
087	-0.84325	0.50595	0.50595	-0.84325	0.50595	-0.84325	
088	-0.40944	-0.40944	-0.40944	-0.40944	-0.40944	-0.40944	
089	-0.32489	-0.32489	-0.32489	-0.32489	-0.32489	-0.32489	
090	-3.52124	-0.26091	-0.22686	0.52224	0.13918	0.61588	
091	-1.46128	-1.24029	-1.24029	0.69335	0.69335	-0.13535	
092	-0.30420	0.87882	0.87882	-0.30420	-0.30420	-0.98023	
093	4.23004	-0.24422	-0.24422	-0.24422	-0.24422	-0.24422	
094	-0.22644	1.51544	-0.22644	-0.22644	-0.22644	-0.92320	
095	-2.69632	-0.05861	-0.05861	-0.05861	-0.05861	-0.05861	
096	-0.29549	-0.50854	-0.43752	3.89434	0.39097	-0.12979	
097	-1.42959	-0.90336	-0.93844	0.49991	-1.14893	-0.79811	
098	-1.75288	-0.42599	0.69137	1.73891	-1.33386	0.41203	
099	-1.77776	-0.12210	-1.07411	1.63703	0.02276	-0.88784	
100	-1.35593	-0.86966	-0.72004	0.51432	-1.01928	-1.13150	
101	-0.78845	0.15693	0.72416	0.53509	1.44266	2.08552	
102	-1.42117	-0.32936	0.50769	0.47129	1.34475	1.12638	
103	-1.31873	-0.24534	0.21467	0.59802	0.82804	2.24644	
104	1.98874	0.72371	0.16474	-0.92376	-0.18828	-1.12969	
105	1.82881	0.48656	-0.68790	-1.69459	1.32547	-0.35234	
106	2.15214	0.44852	-0.21694	-0.90903	-1.46803	-1.01551	
107	2.29435	0.91774	0.36054	-0.95051	0.03277	-1.14717	
108	1.20202	-1.12851	-0.72515	1.56056	1.42611	0.39529	
109	-0.52248	-1.33677	-0.61971	2.02490	1.19846	-0.05578	
110	-0.33006	1.14165	0.12716	-0.70156	-0.60154	-0.88731	
111	-0.12079	0.32521	0.10221	-1.08715	-0.78981	-0.90131	
112	-1.19956	-1.21120	-0.53605	2.00160	1.21004	-0.00058	
113	0.75201	0.55977	0.14784	-0.38310	-0.10847	-1.07882	
114	-0.67030	-0.22895	-0.33928	-0.11861	-0.00827	-0.67030	
115	0.11167	0.26749	-0.09609	-1.65432	-1.08297	-0.66744	
116	-0.62769	-0.94198	-0.70605	1.12407	0.68676	-0.27211	
117	-0.72731	-1.03407	-0.96082	1.06414	0.30154	-0.42227	
118	-0.81657	-0.94349	-0.25724	0.41754	0.24760	-0.21832	
119	-2.05489	-0.99635	-0.44061	0.06218	-0.86403	-0.25537	
120	0.54238	0.24806	0.87874	0.58442	1.04692	1.55146	
121	1.46870	0.59404	0.35107	-0.49928	0.47255	-1.22816	
122	3.60945	0.46219	0.67800	-0.59887	-0.02337	-0.70678	
123	-0.75896	0.48297	-0.11499	-0.46764	0.78962	-0.75896	
124	2.49106	0.61832	-0.05973	0.06942	-1.02838	-0.77008	
125	-0.83395	-0.18344	0.16783	1.01349	-0.36558	-1.31533	
126	-0.41902	0.21227	-0.79781	-0.41902	-0.10337	-0.21385	
127	0.19692	-0.19817	-0.07340	-0.50176	0.35080	-0.95924	
128	-0.59673	-0.12870	-0.36272	0.52653	-0.64354	1.22857	
129	0.52974	-0.05886	-0.05886	-0.73801	0.34863	-0.87384	
130	-0.62270	-0.45829	-0.54049	0.19934	-0.70490	1.26800	
131	-0.26266	0.02129	-0.12068	0.58921	-0.40464	1.01515	

132	1.15327	-1.14901	-1.14901	2.00597	1.06800	0.38584	
133	-0.35840	0.38196	0.01177	0.95406	0.34830	0.75214	
134	0.04607	0.91898	0.43403	-1.74825	-0.87533	0.77349	
135	-0.75950	1.55630	1.16379	-2.05478	-1.07351	0.81053	
136	-0.41815	1.10241	0.49418	-1.71064	-0.57021	0.87432	
137	-0.21782	1.07487	0.48832	-1.73830	-0.63923	0.84708	
138	-1.91387	-1.05894	-0.78692	-0.16515	-0.86464	-0.28173	
139	-1.32041	-0.26950	0.61189	0.61189	0.78139	2.23910	
140	-2.04970	-1.37066	-0.64131	0.36467	-0.71676	0.18862	
141	-0.93271	-0.31090	0.80835	-0.37308	0.22799	2.13488	
142	0.27245	1.73752	0.50377	-1.39824	-0.93558	-0.66570	
143	1.37925	0.87671	0.91746	-0.90252	-0.72595	-0.76670	
144	0.47749	0.31060	0.51458	-1.91463	-1.28414	0.12516	
145	0.31655	0.33367	-0.04848	1.07801	-0.93256	-0.09126	
146	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	
147	1.10571	0.28839	0.07822	-0.29540	-0.13193	-0.57562	
148	1.32108	0.32527	0.21037	-1.09182	-0.65411	-0.80184	
149	1.50990	0.03871	-0.03871	-0.89045	-0.11614	-0.34844	
150	-0.84271	-1.18920	-0.58422	2.00621	1.23073	-0.02873	
151	-0.37161	-0.10378	-0.07030	-0.13726	-0.27117	1.57015	
152	2.34061	-0.17467	-0.68281	0.60023	1.33704	0.47320	
153	-0.57330	0.34183	-0.03499	-1.64994	-1.05779	-0.62714	
154	-0.73388	-0.87931	-0.72350	1.50984	1.28132	-0.66117	
155	-1.04000	0.27507	0.24584	0.29333	-0.01351	0.41388	
156	0.81373	0.57620	0.34308	-0.66857	-1.02486	0.06157	
157	-0.65858	-1.01916	-0.67979	1.37762	1.20793	-0.57374	
158	0.18582	-1.23517	-1.12586	1.71613	1.16959	0.40443	
159	-0.00184	-1.07068	-0.51783	2.87297	1.61984	-0.14926	
160	-1.91466	-0.78949	-0.78949	-0.15189	-1.16455	-0.45194	
161	-1.41509	-0.17413	0.86667	0.58645	1.02679	1.98754	
162	2.40143	0.92247	0.22059	-0.48129	0.24565	-1.20823	
163	-1.71215	-1.00530	-0.88749	-0.18064	-1.12311	-0.33771	
164	-1.29481	0.06394	1.06302	1.02306	1.22287	1.70243	
165	2.21442	0.91896	0.02833	-0.45745	-0.07961	-1.34808	
166	0.72678	1.21492	0.88949	0.56407	0.72678	-1.33424	
167	-1.51265	-0.50899	0.20790	1.21155	1.18766	1.85676	
168	-0.93384	-0.40282	-0.56971	-0.11454	0.17372	2.52540	
169	-1.58988	-0.46673	0.60650	1.72965	1.55493	1.18055	
170	-0.95532	-1.04419	-0.75219	0.66967	0.34594	1.79956	
171	-1.58712	-0.96297	-0.72520	-0.04160	-0.99269	-0.13077	
172	1.03129	0.12355	0.82957	0.27484	1.18258	1.58602	
173	-0.82502	-0.04942	-0.18629	-0.06463	0.40681	-0.26233	
174	-0.60517	-0.21641	-0.51014	-0.70884	0.12915	-0.50150	
175	-0.98060	0.02546	-0.09874	0.17450	-0.50862	-0.38441	
176	2.52610	1.49396	0.62061	0.27656	-0.33213	-1.09963	
177	-0.73480	-1.16482	-0.72728	2.23219	1.19938	-0.45406	
178	0.55012	-0.07969	0.11310	1.68122	0.55012	0.11310	
179	0.75629	-0.91483	-0.17211	2.19889	0.78486	0.08498	
180	0.18932	-1.07282	-0.82371	2.29843	0.68753	0.43842	

181	0.08063	-1.04453	-0.61321	2.33097	0.75573	0.36192	
182	0.78194	1.00697	0.66943	-1.13073	-0.00562	-1.35575	
183	0.53541	0.53541	0.38972	-0.70295	0.46256	-1.14002	
184	-0.62060	-0.25119	-0.25119	0.56150	-0.25119	0.56150	
185	-0.72957	-0.80714	-0.58414	1.14163	0.25935	0.82168	
186	-1.29654	-0.96985	-0.60233	0.17355	-1.58239	-0.19397	
187	-0.88574	-0.81876	0.72165	0.38678	0.18585	1.32442	
188	1.57752	1.26650	0.19524	-0.35766	1.30106	-0.49589	
189	-0.02307	0.87618	0.36707	-1.74070	-0.87951	0.78578	
190	0.86306	0.38848	0.11729	-1.88952	-1.06239	-0.01830	
191	-0.06383	0.77710	0.76492	-0.75852	-0.28016	0.03671	
192	-0.16605	0.12698	0.52745	0.87909	0.40047	-0.70327	
193	0.08138	0.75211	0.94855	-0.59214	-0.41815	-0.09541	
194	-0.01890	0.14437	0.73736	1.04674	0.05843	-0.79236	
195	-0.47564	0.77160	0.15142	-1.15784	0.14453	0.40639	
196	-0.59313	0.05182	-0.25913	0.19003	1.37631	-0.32824	
197	-0.24662	0.48668	0.25511	-1.07255	-0.66344	0.98455	
198	-0.44509	-0.46427	-0.15731	1.39667	0.05371	0.61008	
199	-0.60332	0.08344	0.13374	-0.50927	-0.50709	1.40885	
200	-0.28615	0.35336	0.74706	-0.55501	-0.46667	0.24966	
201	-0.64493	-0.62967	-0.26331	0.82048	-0.64493	0.31674	
202	0.51401	1.41649	-0.22802	-1.68402	-0.98610	0.17708	
203	0.74792	0.76147	-0.50511	-1.53463	-1.35175	-0.14613	
204	0.33284	1.55479	1.23268	-1.69692	-0.80730	1.02306	
205	0.59047	1.47546	0.09720	-1.40195	-0.81196	0.57596	
206	-0.42810	-0.13551	-0.10935	-0.45589	-0.25810	1.52690	
207	0.08909	1.09167	0.07997	-1.79758	-1.02741	0.12099	
208	-0.09604	0.84639	0.52224	-1.61474	-0.27012	0.64229	
209	-0.61209	0.11666	-0.06452	-0.56378	-0.37655	1.49566	
210	-0.97062	-0.86693	-0.50979	0.94182	0.58467	1.33352	
211	-0.97052	-0.91822	-0.46681	1.29476	0.45525	1.08832	
212	-0.75415	-0.75415	-0.37707	2.45101	1.41404	0.65988	
213	0.27314	0.00125	-0.06923	-0.58279	0.33859	-1.14670	
214	-0.28419	-0.76776	-0.41103	1.34884	1.34884	-0.42689	
215	0.58932	0.64174	0.24863	-1.87412	-0.67515	-1.14688	
216	0.13067	0.30327	0.07091	-1.66101	-0.91612	-0.11712	
217	0.01470	0.18988	-0.00784	-1.14671	-0.73192	-0.01066	
218	-0.80161	-0.04429	0.61299	0.68444	0.49868	1.40604	
219	0.71551	-0.04375	0.05276	-3.64061	-0.75797	0.20075	
220	-0.37343	-0.56573	-1.09646	1.03416	-1.62719	0.48804	
221	1.02021	0.02755	-0.43295	-2.34663	1.61376	-0.31892	
222	0.19224	0.79567	1.46532	-0.97412	-0.81591	-0.29711	
223	-1.56377	-0.94730	-0.86511	0.08014	-1.23499	-0.24864	
224	-1.61919	-0.87216	-0.53599	0.06163	-1.05892	0.17368	
225	-1.07446	0.03280	0.72998	0.93503	1.38614	1.75523	
226	-1.53681	-0.86437	0.53655	0.76070	1.23702	2.02154	
227	1.38709	0.90039	0.25146	-0.20819	0.87335	-1.20863	
228	1.44006	1.29720	-0.13143	-0.30287	0.32572	-1.30291	
229	-0.88549	-0.52406	1.28306	1.46377	-1.87941	0.19878	

230	-1.67414	0.18601	-0.82565	-1.15199	-0.85828	0.61026	
231	-1.31262	-0.79277	-0.22960	0.37689	-1.31262	-0.87941	
232	-1.33551	-0.67933	0.44002	0.09263	1.21200	2.40856	
233	-1.14191	-1.27298	-0.19168	0.69301	0.72578	0.59471	
234	-0.99928	-0.08082	0.72741	0.94784	0.83763	2.27042	
235	0.46258	0.56892	-0.78987	-1.12071	0.68707	-0.95529	
236	1.45657	0.37151	0.46586	0.74892	-0.90225	-0.54842	
237	1.76760	1.03437	-0.19640	0.40589	0.77250	-1.11293	
238	0.83934	1.08192	0.37843	-0.93152	2.00375	-1.10133	
239	0.17686	0.87166	0.66638	-1.73386	-0.45478	-0.73902	
240	0.20801	-1.01561	-0.41909	1.35516	0.33037	0.85042	
241	-0.91651	-0.86904	-0.60457	0.27702	0.50759	1.71470	
242	-0.79637	-0.61153	-0.51593	0.33174	0.40822	1.58732	
243	-0.63870	-0.24304	-0.38435	0.46348	0.29391	1.48088	
244	-0.95116	-1.14394	0.19778	-0.52705	-0.07980	0.10525	
245	-0.14038	-0.70963	0.16731	-0.29423	0.36731	1.55196	
246	-0.85638	-0.46183	-0.91979	-0.29978	-0.22228	1.42636	
247	-0.94266	-0.77577	-0.68425	1.28075	-0.45275	1.75988	
248	-0.54419	-0.67223	-0.37346	0.87497	0.60821	1.55788	
249	1.05810	0.64838	-0.88807	-0.06862	-0.02765	-0.06862	
250	0.60729	1.09622	1.01902	-0.52495	-0.80801	-0.42202	
251	0.33448	1.10285	1.27824	0.60174	-0.54244	-0.25848	
252	-0.24097	-0.40211	-0.52419	-0.66580	-0.13843	-0.81229	
253	-1.91466	-0.78949	-0.78949	-0.15189	-1.16455	-0.45194	
254	-1.41509	-0.17413	0.86667	0.58645	1.02679	1.98754	
255	2.39357	0.94594	0.19717	-0.50167	0.24709	-1.20053	
256	-3.14344	-0.62868	-0.62868	0.72540	0.72540	0.14508	
257	-1.15382	-0.55554	0.12820	0.55554	1.06835	2.09398	
258	-1.37299	-1.37299	-0.05702	-0.23248	-0.93434	0.03070	
259	-0.29129	0.23303	-1.80601	0.11651	-1.51472	0.29129	
260	-1.53127	-0.36425	-0.25816	-0.08133	-1.35445	-0.04597	
261	-1.19890	-0.59140	-0.69861	0.90944	-1.05596	-0.01965	
262	-2.04407	-0.68044	-0.24408	0.57408	-0.08045	0.35590	
263	-2.09589	-0.77065	-0.82827	0.43934	-0.65541	0.61220	
264	-2.37248	-0.88179	-1.04233	-0.03325	-0.60659	0.90702	
265	-3.32682	-0.37166	-0.55296	0.31727	-0.29914	0.48044	
266	-3.08679	-0.56051	-0.40262	0.11616	-0.15450	0.45450	
267	-2.62318	-0.90908	-0.80705	0.37648	-0.07244	0.07040	
268	-2.65896	-0.75152	-0.67523	0.49466	0.36749	-0.03942	
269	-2.50543	-0.12217	-0.45402	0.99402	0.36050	0.20966	
270	-1.67130	0.40195	-1.29049	1.62899	0.10577	-0.44427	
271	-0.43612	1.80681	1.47452	-0.31151	-0.31151	-0.18691	
272	0.95303	1.65899	1.30601	-0.65496	0.52162	-0.41965	
273	0.68646	1.74256	1.58415	-0.58085	0.68646	-0.36963	
274	0.23157	-0.27898	0.15863	-0.20604	0.81506	1.21621	
275	-0.90874	0.31065	0.07839	0.42679	0.83325	1.38489	
276	-1.66766	-0.20788	0.91929	0.64211	0.78994	1.41820	
277	-1.86846	-0.37881	0.39003	0.83852	1.35109	1.22295	
278	-2.25097	-0.36573	0.31295	0.57688	1.16130	1.42524	

279	-2.04357	0.15988	-0.32380	0.32111	0.99290	1.63781	
280	-1.45889	1.46669	2.24684	-0.44468	-0.01560	0.64752	
281	-0.82831	1.59883	1.32914	-0.01926	0.52010	0.71273	
282	-0.06960	1.88791	1.67041	0.06090	-0.24360	-0.67860	
283	1.24269	1.43839	1.66670	-1.00785	1.17745	0.03587	
284	1.36873	-0.87246	-0.60565	0.72838	1.47545	-0.07203	
285	-0.01087	-1.18568	-0.27194	0.51125	0.77232	0.03263	
286	1.17746	-0.94072	-1.06532	0.63753	0.38833	-0.40079	
287	0.88787	1.21444	0.72458	-0.29595	0.23472	-1.03074	
288	2.11584	0.54944	0.35665	-1.08924	-0.48678	-1.11334	
289	2.26022	0.64750	-0.15885	-0.73943	-0.07821	-1.38452	
290	2.26856	0.82013	0.38815	-0.45040	-0.50123	-1.65742	
291	3.13493	0.49240	0.21998	-0.55642	-0.62453	-1.30559	
292	2.97405	0.60970	0.40491	-0.30252	-0.63763	-1.28922	
293	2.78479	0.44092	0.09282	-0.32489	0.37130	-0.11603	
294	2.88272	-0.24553	-0.90028	-0.24553	-0.82753	-0.13640	
295	2.35936	-1.07535	-1.10745	-0.72225	0.08025	0.78645	
296	0.43654	-1.62490	-0.37186	-0.45270	-1.01859	0.51738	
297	1.18905	1.28166	0.78772	-0.85873	-0.00463	-1.09540	
298	0.79669	0.72329	0.46307	-0.71128	0.50977	-1.04491	
299	0.47412	0.06759	-0.05530	-0.74546	0.17159	-0.89672	
300	0.47717	0.54821	1.63754	-1.03841	0.16931	-0.89632	
301	1.36334	-0.19802	-0.88350	0.48745	-1.60706	-0.84542	
302	-1.08185	-0.00829	1.08272	-1.08185	0.57649	0.33210	
303	0.89230	0.12902	0.60153	-0.47068	0.12902	-0.23443	
304	-0.94857	-0.24009	-0.71241	1.91158	1.17686	0.86198	
305	-0.52212	-0.04877	-0.32130	0.55368	-0.47909	-0.79466	
306	-1.15557	-0.42744	0.19282	0.39508	0.74566	-0.38699	
307	-2.52639	-0.58999	-0.83204	0.55974	-0.52948	-0.46897	
308	0.56899	-0.57590	0.13750	-0.57590	0.51721	-0.57590	
309	2.76321	0.03084	-0.69190	0.10136	-0.12780	-0.49799	
310	0.60348	-0.59153	0.63336	-0.14340	1.44000	1.58938	
311	-2.79743	0.77223	0.01070	0.36767	-0.20347	-0.39385	
312	0.38074	-0.22413	-0.38028	0.29281	0.76731	-0.66225	
313	3.33535	-0.40887	-0.13083	-0.27480	0.44832	-0.04511	
314	0.31745	-0.32925	-0.17137	0.76064	0.29083	1.08590	
315	-0.59601	-0.55692	-0.33220	1.85642	0.99660	0.55692	
316	1.38738	0.63524	0.34072	-2.33254	-1.31760	0.45853	
317	0.45117	-0.36269	-0.22073	0.40859	0.03241	1.12782	
318	0.84677	-0.06594	-0.07489	-0.65474	-0.53841	0.99173	
319	-2.47744	-0.82686	-0.33546	1.61658	1.13874	-0.10785	
320	0.92720	-0.06198	-0.00923	0.14903	-0.41810	1.04591	
321	-0.18048	-0.74982	-0.48793	0.82156	0.19528	1.06069	
322	-0.65424	1.41178	-1.57247	0.26399	2.10046	-0.65424	
323	-0.65424	1.41178	-1.57247	0.26399	2.10046	-0.65424	
324	-0.15752	1.53022	0.74260	-0.72010	-0.15752	-0.94513	
325	2.45465	-0.49714	-0.34178	1.67786	1.21179	0.12428	
326	-0.87670	-0.35068	-0.52602	1.22738	-1.05204	-0.70136	
327	-0.84192	-0.84192	0.00707	0.57307	0.29007	0.14857	

328	-1.22506	-0.85754	-0.73504	2.45013	-0.61253	0.49002	
329	-1.63585	0.13263	-0.97267	0.79582	-1.85691	-0.53054	
330	-2.03925	-1.22355	-0.13595	1.22355	-0.67975	0.40785	
331	-1.11572	-0.83146	-0.83146	0.02131	0.30557	-0.97359	
332	-1.38323	-0.76295	-0.63889	1.22196	-0.39078	0.35356	
333	-1.61548	-0.62641	-0.46156	-0.95610	0.19781	0.52750	
334	-1.31643	0.93113	-0.19264	-0.99535	-1.15589	-0.51372	
335	-1.34168	0.78004	-0.09360	-1.34168	0.15600	-0.46802	
336	-0.22252	-0.09889	-0.71702	-1.08789	-0.09889	-0.84064	
337	2.32110	-0.69005	-0.43912	-1.44284	-0.18819	-0.94098	
338	0.74070	-0.23604	1.71745	2.69420	-0.88721	-0.07325	
339	-1.74719	-0.87359	-0.57473	0.29886	-1.01153	0.34484	
340	1.88941	-0.66355	0.61293	-0.09133	-0.70756	-0.86162	
341	-3.28184	-0.29560	-0.44642	0.76013	-0.53691	0.53390	
342	-3.51119	-0.18969	-0.45541	-0.04207	0.00221	0.43031	
343	-0.51419	-0.48691	0.33142	-0.29596	1.06793	1.83171	
344	-1.47209	-0.51500	0.41929	0.10026	0.78390	1.64983	
345	2.18771	0.26340	-0.14668	-1.21925	1.36752	0.70505	
346	0.67830	0.67830	0.07941	0.88661	0.75642	-1.56102	
347	2.14817	0.54302	-0.31078	-0.34493	0.98699	-1.26704	
348	0.89490	0.54849	0.20207	0.82562	0.94109	-1.36834	
349	-1.81063	0.41191	0.32301	1.89361	0.35264	-1.39576	
350	1.93894	0.91844	0.67105	0.51643	-0.04020	-0.93700	
351	0.89247	0.81737	0.01627	0.74226	0.81737	-1.56089	
352	-0.22232	-1.23864	-0.79400	1.42920	0.85752	0.41288	
353	-0.96540	-1.13965	-0.64078	2.17822	1.05873	0.18272	
354	-0.83683	-0.66339	-0.31652	0.98425	0.20378	1.07097	
355	-0.83168	0.47670	0.37160	-1.06976	-0.24612	-0.92391	
356	-0.70014	0.15116	-0.08812	-1.21093	0.55611	-0.89802	
357	0.88546	-0.64120	-0.64120	-0.03053	1.80146	-0.64120	
358	1.17459	-1.12870	-0.76881	1.53448	1.50749	0.35584	
359	-1.54707	0.42142	-0.21625	-1.04801	-0.77076	0.94820	
360	1.61767	0.10090	0.59777	-0.04293	-0.59646	1.07285	
361	-0.08698	-0.68430	-0.92410	2.13225	1.64393	-0.69302	
362	-0.18193	2.02307	1.49142	0.19282	0.93364	-0.94889	
363	-1.57923	-1.00090	-0.67452	0.98601	0.48785	0.08703	
364	0.64116	-0.89264	-0.89264	1.92238	1.51971	-0.89264	
365	-0.49064	-0.55065	-0.28058	0.49964	1.66997	0.90976	
366	-1.22599	-1.02023	-0.78017	0.14574	-1.15740	-0.06001	
367	1.61130	-0.87285	1.40244	1.34548	-0.43140	-1.05323	
368	0.86675	0.25409	0.72929	0.33656	1.22413	1.56974	
369	3.71120	0.80527	0.34439	-0.87559	-0.25882	-0.55704	
370	-1.60447	0.30591	-0.48418	0.56535	0.56535	-0.67089	
371	-0.71430	0.39061	1.34246	-0.56122	0.61883	-1.05663	
372	-0.79672	-0.65995	-0.61037	-0.79672	-0.23767	-0.65397	
373	-0.69334	0.06620	0.79082	0.84604	-1.16101	-0.09494	
374	-0.79311	0.54887	-0.11374	-0.31947	-0.00849	-0.83617	
375	1.47891	1.00256	0.25082	-0.39670	0.42201	-1.28241	
376	-0.25631	-2.01494	-0.89241	-0.06922	-1.31648	1.41501	

377	1.52547	1.29427	1.73817	-1.15185	-1.61425	-0.24553	
378	0.40778	-0.69737	-1.08622	0.90407	2.30598	0.07521	
379	-0.72581	0.84314	1.12049	0.14453	0.06450	-1.07623	
380	-0.63807	-0.63807	-0.63807	1.48884	1.48884	1.48884	
381	0.42589	-0.05113	-0.22030	-1.00067	-0.04919	-1.00262	
382	0.27111	-0.19384	-0.24623	0.45448	-0.31172	0.98493	
383	0.17430	0.92513	0.71061	-3.15082	-1.59552	0.33519	
384	-1.10945	-0.40504	-0.95851	1.45663	0.34969	0.75221	
385	-1.01283	0.54537	0.70656	-0.31432	-0.55612	-0.66358	
386	0.03277	0.08976	0.51722	-0.62266	0.26074	-0.50867	
387	-0.68451	0.37084	0.95714	-1.09493	-1.09493	0.37084	
388	-0.35541	0.01015	-0.35541	-0.88346	-0.72098	-0.76160	
389	0.20637	-0.02460	0.00552	-0.16185	-0.20034	1.15539	
390	-0.40739	0.65232	0.30575	-1.58375	-0.46404	-0.89726	
391	0.41198	-0.76511	-0.98083	1.71100	1.08728	-1.18717	
392	1.25695	0.32044	-0.79095	0.47840	0.00451	-0.72889	
393	-0.34223	-0.57231	-0.16968	0.14667	-0.16968	0.75061	
394	-0.19844	0.26111	-0.15666	-0.69978	-0.24022	0.84600	
395	0.27188	0.12579	0.11836	0.03169	0.22979	0.30655	
396	0.33289	0.16093	0.07616	-0.12727	0.20211	0.38375	
397	-0.44679	-0.60050	-0.36994	2.73910	0.81778	-0.05554	
398	1.36572	-1.08865	-0.70515	-0.92566	1.62458	0.49327	
399	0.44520	-1.27301	0.08688	1.36043	0.57471	1.33885	
400	-0.54823	-0.54412	-0.54458	-0.52450	-0.54686	-0.61439	
401	0.15459	-0.19585	-0.20715	-0.07715	-0.20715	-0.03758	
402	0.84353	-0.55939	-0.09767	1.25198	0.87905	0.75474	
403	0.96709	-1.61533	-0.66668	-0.45587	0.22925	-0.50857	
404	1.64709	0.14738	-0.99032	-0.47318	0.66452	-0.62832	
405	0.26492	-0.17256	0.16770	0.31353	-0.26978	-1.82529	
406	1.25957	0.78904	0.53568	-1.09307	-0.65874	-1.45502	
407	0.60643	1.07291	1.64705	-0.03947	-0.47007	-1.00832	
408	1.55068	-0.48533	-0.58002	0.58002	-0.05918	-0.60370	
409	-0.19495	-0.81188	-0.24430	0.19988	-0.71317	-0.78721	
410	-1.87691	-0.88223	-0.57950	1.43147	-0.79574	0.26380	
411	-1.98195	-1.17420	-0.76047	0.12608	-0.20883	0.28370	
412	-1.69626	-0.62775	-0.56610	-0.60720	-0.13459	-0.34007	
413	-1.30664	-0.77725	-0.60880	-0.72912	0.13716	0.11309	
414	-1.83097	-0.77843	-0.53723	1.06350	0.05481	-0.20831	
415	-1.80670	-0.71629	-1.07349	1.01333	0.12972	-0.17108	
416	-1.84657	-1.16910	-0.87876	-0.04645	-0.00774	0.10839	
417	-1.72922	-0.48425	-0.86873	0.04668	-0.44764	-0.85042	
418	-2.16608	0.03225	-0.44564	-1.01912	0.12783	-1.30586	
419	-0.58201	-0.62088	-0.27108	-0.73747	-0.05732	-0.83464	
420	-0.03720	-1.63190	-0.94087	0.22857	0.70698	-1.47243	
421	3.03692	-0.67206	-0.58305	-0.22699	-1.02813	-0.64239	
422	2.18723	-0.97743	-2.67730	0.83095	-0.37463	0.43913	
423	-3.85310	0.15468	-0.19687	0.29531	0.08437	-0.05624	
424	4.06542	-0.24512	0.06369	-0.37379	-0.01351	0.02509	
425	0.89348	0.84754	0.09723	-1.32683	-0.94401	-0.91339	

426	0.62757	1.19479	0.36578	-1.64129	-1.45221	-0.92863	
427	1.43244	0.76557	0.04534	-1.55514	-0.40812	-0.75490	
428	0.62991	0.74091	-0.14707	-0.09157	-0.53556	-0.92405	
429	3.31510	0.48669	0.36432	-0.17521	0.06952	-0.13071	
430	3.14783	0.05266	0.37325	-0.17250	0.20532	-0.06182	
431	2.08988	0.27704	-0.58885	-0.71255	-1.09644	-1.60404	
432	3.73750	-0.17386	-0.63364	-0.41551	-0.65289	-0.90096	
433	3.78955	-0.32373	-0.64365	-0.47607	-0.65888	-0.82646	
434	-0.48823	-0.09813	-0.11032	2.31562	1.20626	-0.02499	
435	1.52730	0.23776	-0.48761	-0.48761	-0.64880	-0.89059	
436	1.23497	-0.56790	-1.10876	-0.56790	-0.74819	-0.92848	
437	-4.04918	0.08876	0.10242	0.15705	0.34824	0.22533	
438	1.33989	1.08603	0.22926	-1.26214	-2.02371	-0.64336	
439	0.10250	0.41570	-0.11104	-0.79439	-0.85134	-0.75168	
440	-0.32046	-0.40008	0.27667	-1.47494	-0.20103	1.27191	
441	-0.31781	0.20517	0.28563	-1.52470	-0.51896	1.29137	
442	-1.31325	-0.33594	-0.18324	-1.16055	-0.15270	0.27486	
443	-1.18770	-0.38628	-0.12983	-1.28387	-0.54656	0.67159	
444	0.64731	-1.09952	-0.49376	1.94336	0.95724	0.68958	
445	-2.33273	-0.54119	-0.79001	1.84752	1.54893	0.35457	
446	-0.75058	-0.26875	0.02034	0.72702	-0.02248	1.16602	
447	-0.70607	-0.17751	0.05185	0.76989	0.19147	1.15883	
448	-0.94180	-0.40940	0.02715	1.00675	0.30399	1.15582	
449	-1.04771	-0.52385	0.06548	1.13502	0.32741	1.08045	
450	-1.27714	-0.69769	0.13007	1.09976	0.23650	1.04063	
451	-1.47542	-0.76187	0.61917	1.20611	0.02071	1.05650	
452	-1.50029	-0.84406	1.00976	1.05078	-0.47494	0.51759	
453	-0.01259	-0.23292	-0.29588	-0.23292	-0.23292	-0.39031	
454	-0.18257	0.22314	0.87227	0.38542	-0.04733	-0.34485	
455	-0.25078	1.50167	-1.09679	-0.41998	-0.84299	-1.09679	
456	-0.04762	1.09530	0.47621	-1.71438	-0.66670	0.80957	
457	0.18787	1.04399	0.52080	-1.71462	-0.85850	0.80618	
458	-0.12092	0.96321	0.25435	-1.33015	-0.70468	1.13000	
459	0.14203	0.75753	0.14203	-1.79913	-0.89956	0.85222	
460	0.75314	1.50234	0.04337	-1.69161	-1.02127	0.12223	
461	0.10146	-0.18031	-0.28906	-1.07013	-0.55601	-0.23468	
462	-0.06492	0.12629	0.11087	-1.37571	-0.84523	-0.44119	
463	0.17625	1.35129	1.16035	-1.12216	-0.51114	-0.55814	
464	0.22009	0.62570	0.05030	-1.39603	-0.89296	-0.28298	
465	-0.32885	-0.24657	-0.00521	-1.06665	-0.25480	2.06557	
466	-0.45786	-0.02000	0.15977	-1.07840	-0.42017	1.65023	
467	-0.63151	0.36164	0.21775	-0.84207	0.40375	1.56536	
468	-0.45947	0.27028	0.00000	-0.80814	-0.28109	1.41627	
469	-0.16333	-0.29130	-0.19533	-1.45725	-0.54724	1.28698	
470	-0.39359	0.06173	0.18890	-1.66113	-0.83661	1.01341	
471	-0.30298	1.10899	0.89047	-1.27792	-0.06345	0.67195	
472	-0.19891	0.69018	0.03696	-1.70492	-0.90202	0.90791	
473	0.18165	-0.06296	1.04236	0.25413	0.51688	1.97556	
474	0.06338	-0.40582	0.46674	-0.44698	-0.23295	1.52041	

475	-0.36562	-0.50220	1.45198	0.55894	0.94767	1.66211	
476	-0.37641	0.45370	1.16931	0.59682	0.79719	1.59868	
477	-0.31380	-0.21619	1.03315	0.50608	1.00387	1.73592	
478	-0.32892	-0.07590	1.30259	0.47375	0.83146	1.38112	
479	-0.34574	1.64719	0.97533	0.31101	0.43180	1.30749	
480	0.12039	0.25820	1.89011	1.20834	0.30897	1.67252	
481	-0.03600	-0.59857	0.87536	2.36055	1.68546	-0.38479	
482	1.19229	-1.88460	-0.60255	0.50854	1.10682	0.67948	
483	-0.55940	-0.55940	-0.55940	2.95207	2.00453	-0.55940	
484	-0.53457	-1.20600	-0.58358	2.03353	1.25427	-0.12779	
485	-0.54263	-1.21195	-0.57671	2.02025	1.26087	-0.15077	
486	-0.72575	0.84256	1.12093	0.14415	0.06462	-1.07620	
487	-1.28671	-0.82222	-0.49258	0.88590	0.59372	1.46277	
488	-0.01745	-0.77872	-0.05180	0.88690	0.65795	0.48623	
489	-0.34272	-0.72186	0.23345	1.45747	0.10807	0.37974	
490	0.53779	0.04091	0.27474	0.37217	0.29423	-0.30657	
491	-0.50132	0.32757	-0.36583	0.98910	-1.46970	0.37938	
492	-0.61468	0.29704	0.44409	-0.58527	0.29704	-1.14407	
493	-0.13810	-0.75441	-0.54897	1.77932	0.56952	0.70647	
494	-0.44476	0.01801	-0.04809	0.03123	-0.24642	1.57162	